

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) <u>1</u>	STN _____
Searcher Phone #: _____	AA Sequence (#) <u>2</u>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>1/8/01</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>1/13/01</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <u>03</u>
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2001, 16:23:06 ; Search time 2662.02 Seconds
(without alignments)
4342.942 Million cell updates/sec

Title: US-09-119-209-1

Perfect score: 2259

Sequence: 1 GAATTCACAGTGTGTGCTT.....CCGCCAGCACACTGGAATTC 2259

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_da1: *
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3: gb_cm: *
4: gb_ov: *
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84: gb_htg24: *
85: gb_pr8: *

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2259	100.0	2259	81 AR060685	AR060685 Sequence
2	2258	100.0	2259	85 MPMPLNHR	X16070 Human mRNA
3	2161	95.7	2354	85 HUMMLNHR	M25280 Human Lymph
4	2127.8	94.2	2323	53 HSLLEU8	X17519 Human mRNA
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6	2087.6	92.4	2330	81 AR016679	AR016679 Sequence
7	2087.6	92.4	2330	81 AR040718	AR040718 Sequence
8	2087.6	92.4	2330	81 AR054061	AR054061 Sequence
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11	1351.2	59.8	1510	85 PHU52074	U52074 Papi hamad
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13	1085.4	48.0	1119	85 PTU73729	U73729 Pongo pygma
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ALIGNMENTS

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LOCUS Sequence 1 from patent US 5840844.
DEFINITION AR060685
ACCESSION AR060685
VERSION AR060685.1 GI:5987135
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2259)
AUTHORS Lasky,L.A., Rosen,S.D., Stachel,S.E. and Slinger,M.S.
TITLE Soluble lymphocyte homing receptors
JOURNAL Patent: US 5840844-A 1 24-NOV-1998;
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ORIGIN

Query Match 100.0%; Score 2259; DB 81; Length 2259;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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LOCUS Human mRNA for pln homing receptor homologue (peripheral lymph node).
X16070
ACCESSION X16070
VERSION 1.1
KEYWORDS lymphocyte adhesion receptor; lymphocyte homing receptor; transmembrane protein.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

REFERENCE	Primates: Catarrhini, Hominoidea: Homo.			
AUTHORS	Bowen, B.R., Nguyen, T., and Lasky, L.A.			
TITLE	Characterization of a human homologue of the murine peripheral lymph node homing receptor			
JOURNAL	J. Cell Biol. 109 (1), 421-427 (1989)			
MEDLINE	89308881			
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 REFERENCE
 1 (bases 1 to 2354)
 Siegelman, M.H. and Weissman, I.L.
 Human homologue of mouse lymph node homing receptor: evolutionary
 conservation at tandem cell interaction domains
 Proc. Natl. Acad. Sci. U.S.A. 86 (14), 5562-5566 (1989)
 JOURNAL
 MEDLINE
 89315837
 COMMENT
 Draft entry and computer-readable sequence for [1] kindly provided
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ORIGIN

Query Match 95.7%; Score 2161; DB 85; Length 2354;
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Matches 2200; Conservative 0; Mismatches 10; Indels 3; Gaps 3;

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VERSION X17519.1 GI:34344
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 2323)
AUTHORS Camerini, D., James, S.P., Stamenkovic, I. and Seed, B.
TITLE Leu-8/TOI is the human equivalent of the Mel-14 lymph node homing
JOURNAL Nature 342 (6245), 78-82 (1989)
MEDLINE 90044046
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QY 524 TATCAGAGAAACAAGATGCAAGGCAAAATGGAACATGACCCCTGCCAACAATCTAAAGGC 583
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Db 487 TATCAGAGAAACAAGATGCAAGGCAAAATGGAACATGACCCCTGCCAACAATCTAAAGGC 546
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QY 704 GCTTGTATTCAGTGTGAGGCTTTGGAGGCCCAAGAGCTGGTATCCATGAGAGCTGTACTCA 763
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Db 667 GCTTGTATTCAGTGTGAGGCTTTGGAGGCCCAAGAGCTGGTATCCATGAGAGCTGTACTCA 726
QY 764 CCCCTTTGGAACCTTCAGCTTCAGCTCAGAGTGTGCTTGAAGTGGCTGCTTAAGAAACAAA 823
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QY 884 AACCTGCAAGTATTCAGTGTGAGGCTCTATATAGACACAGATTTGGGATCATGAACTG 943
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QY 944 TAGCATCCCTTGGCCAGCTTACGTTTACCTGTGATGATACCTTCAATCTGCTCAGAGAG 1003
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Db 907 TAGCATCCCTTGGCCAGCTTACGTTTACCTGTGATGATACCTTCAATCTGCTCAGAGAG 966
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QY 1124 CCCCTCTTCAATTCAGTGGCAGTATGTTACTGATTTCTGCGTTGGCATTTATCAT 1183
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Db 1087 CCCCTCTTCAATTCAGTGGCAGTATGTTACTGATTTCTGCGTTGGCATTTATCAT 1146
QY 1184 TTGGCTGCAAGGAGATTTAAAAAAAGCAAGAAATTCACAGAGAAATGATTAATCAACCATTA 1243
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Db 1147 TTGGCTGCAAGGAGATTTAAAAAAAGCAAGAAATTCACAGAGAAATGATTAATCAACCATTA 1206
QY 1244 TTTAATGCCCCCTTGTGTAAGAAATTTCTTGAATATCTAATAAATCATGATCTTTTAA 1303
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Db 1207 TTTAATGCCCCCTTGTGTAAGAAATTTCTTGAATATCTAATAAATCATGATCTTTTAA 1266
QY 1304 TCCCTTCATGAAAGCTTTGTGTGTGGGACGCTCTACGTCATCAACATGAAAGTGTG-TTCC 1362
| | | | |
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QY 1542 GACTTGTCTCTTCTTGTGACTCTGTTTTCAGTTTCAATTCAGTGTGACTGATGAGAGAG 1601
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Db 1507 GACTTGTCTCTTCTTGTGACTCTGTTTTCAGTTTCAATTCAGTGTGACTGATGAGAGAG 1566
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QY 1782 AAGAGTCAATTTGACAGTGTACCTCGCGCTGTGGAATTTGAGACATCTTAACTGG 1841
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Db 1741 AAGAGTCAATTTGACAGTGTACCTCGCGCTGTGGAATTTGAGACATCTTAACTGG 1800
QY 1842 CTTCAAGGCTCCCACTCTTCTTCAAGCCACTCTCTTTTTCAGTGGGCTGACTCAGACC 1901
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QY 2022 TTCTTTTATCAGATATTATTATGTAAGAAAAATCACTGAAATGCTAGCTGAAGTGACA 2081

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Db 2100 AATGCTCTCTCTTCCCTCGCCCGCAAGCTTTTATCCACTTACCTAGATTCATATATTC 2159
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Db 2160 TTTAAATTTCTATCTCAGGCTCTCCCTCAACCCAC 2193

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AR016679 2330 bp DNA PAT 05-DEC-1998
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DEFINITION AR016679
ACCESSION AR016679.1 GI:3972956
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SOURCE
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REFERENCE 1 (bases 1 to 2330)
AUTHORS Tredder,T.F. and Speerfijn,O.G.
TITLE Anti-LAM 1-3 antibody and hybridoma
JOURNAL Patent: US 5776775-A 1 07-JUL-1998;
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Query Match 92.4%; Score 2087.6; DB 81; Length 2330;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 2161; Conservative 0; Mismatches 24; Indels 9; Gaps 5;

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Qy 164 GCACTTATGAGACATCTTCAAGTTGTGGGGTGGACAATGCTGTGTGATTTCTGGC 223
Db 127 GCACTTATGAGACATCTTCAAGTTGTGGGGTGGACAATGCTGTGTGATTTCTGGC 186
Qy 224 ACATCATGAGACCTGCTGAGACTTACATTTATTTGAAAAACCATGAACTGGCAAG 283
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Qy 344 AATGAGTATCTGGAGAAAGCTGCGCTTCAGTCTTCTTACTAGTAGAATCCG 403
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Qy 404 GAGAGTATGAGAAATATGAGCTGAGGTGGAGACCAACAATCTCTCACTGAAGAAGAGA 463
Db 367 GAGAGTATGAGAAATATGAGCTGAGGTGGAGACCAACAATCTCTCACTGAAGAAGAGA 426
Qy 464 GAACCTGGGAGATGCTGAGCCCAACAAGCAAGAAAGAGAGACCTGCGTGGAGATCTA 523
Db 427 GAACCTGGGAGATGCTGAGCCCAACAAGCAAGAAAGAGAGACCTGCGTGGAGATCTA 486

Qy 524 TATCAGAGAAAACAAGATGAGGCAATGAGAGTACGCTGCGACAACATAAGGC 583
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Qy 584 AGCCCTCTGTACACAGCTTTTGGCAGCCCTGGTCATGACAGTGGCCATGAGAAATGTGT 643
Db 547 AGCCCTCTGTACACAGCTTTTGGCAGCCCTGGTCATGACAGTGGCCATGAGAAATGTGT 606
Qy 644 AGAATATCAATATATGCAACCTGCACTGATGATGGGGTACTATGGGCCCCAGTGCA 703
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Qy 704 GCTTGTGATTCAGTGTAGGCTTTGAGGCCCCAGAGCTGGGTACATGAGACTGTACTCA 763
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Qy 764 CCCCTTTGGAACCTTCACCTTCACCTGAGCTGCTTCAGCTGCTGTGAGAGACAAA 823
Db 727 CCCCTTTGGAACCTTCACCTTCACCTGAGCTGCTTCAGCTGCTGTGAGAGACAAA 786
Qy 824 CTTTAACTGGGATGAGAAACACCTGTGAGCAATTTGGAACGTCATCTCCAGAAC 883
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Qy 944 TAGCATCTCCCTGGCCAGCTTCACCTTACCTGTGATGATGATCTTCATCTGCTCAGAG 1003
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Db 1387 CTCATTTATCCCTCAACCCCCAGCCACAGGTGTTTATACAGCTACACTTTTGTCTTT 1446
Qy 1483 CTGAGAGAAAACAATTAAGCAT -AAGGAAAGATTCATGTGGAATATTAAGATGGCT 1541
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Db 1507 GACTTGTCTCTTCTTCTGACGCTTGTTCAGTTCATGAGTGTCTACTTATGATGACAG 1566
Qy 1602 ACACTTCTAATGAAGTCAAAATTTGATACATATGTAATATGAGTCACTTTCTTGA 1661

QY	104	AACTGAGAAAGGACCAACAAAGCCATGATATTTCCATGAAATGTCCAGAGCACCCAGAG	16
Db	67	AACTAGAGAGAGACCAACCAAGCCATGATATTTCCATGAAATGTCCAGAGCACCCAGAG	12
QY	164	GGACTTATGAAACATCTTCAAGTTGTGGGGGTGGACAAATCTCTGTGTGGATTTCTGGC	22
Db	127	GGACTTATGAAACATCTTCAAGTTGTGGGGGTGGACAAATCTCTGTGTGGATTTCTGGC	18
QY	224	ACATATGGAACCTTACTCTGGACTTACATTTATTCGAAAAACCATTAACTGGCAAG	28
Db	187	ACATATGGAACCCACTGCTGGACTTACATTTATTCGAAAAACCATTAACTGGCAAG	24
QY	284	GGCTGGAAGATTTCCGGAGACAATTACACAGATTTAAGTTGCCATACAAACAGCGGA	34
Db	247	GGCTGGAAGATTTCCGGAGACAATTACACAGATTTAAGTTGCCATACAAACAGCGCGA	30
QY	344	AAATTGATTCGAGAGAAGCTGTGCCCTTCACTGCTCTTACTACTGGATGGAAATCG	40
Db	307	AAATTGATTCGAGAGAAGCTGTGCCCTTCACTGCTCTTACTACTGGATGGAAATCG	36
QY	404	GAACTGGAGGAATATGACGCTGGGTGGGAACCAAAATCTCTCACTGAAAGCAGA	46
Db	367	GAAATATGAGAGAAATATGACGCTGGGTGGGAACCAAAATCTCTCACTGAAAGCAGA	42
QY	464	GAACTGGGGAGTGTGAGCCCAACAAAGAAAGAAAGAGAGACTGCTGGAGATCTA	52
Db	427	GAACTGGGGAGTGTGAGCCCAACAAAGAAAGAAAGAGAGACTGCTGGAGATCTA	48
QY	524	TATCAAGAGAAACAAAGATGCGAGGCAATAGAACATGACCGCTGCCACAAATTAAGGC	58
Db	487	TATCAAGAGAAACAAAGATGCGAGGCAATAGAACATGACCGCTGCCACAAATTAAGGC	54
QY	584	AGCCCTCTGTTACACAGCTTCTTGTGCAGCCCTGGATGATGACAGTGGCCATGAGAAATGT	64
Db	547	AGCCCTCTGTTACACAGCTTCTTGTGCAGCCCTGGATGATGACAGTGGCCATGAGAAATGT	60
QY	644	AGAAATCATCAATAATACACACTGCACTGTGTGATGTGGGTACTATGAGGCCCAAGTGTCA	70
Db	607	AGAAATCATCAATAATATACACTGTCAACCTGTGATGTGGGTACTATGAGGCCCAAGTGTCA	66
QY	704	GCTTGTGATTCAGTGTGAGCCTTTGGAGGCCCAAGTGGGTCACTGAGACTGTACTCA	76
Db	667	GCTTGTGATTCAGTGTGAGCCTTTGGAGGCCCAAGTGGGTCACTGAGACTGTACTCA	72
QY	764	CCCCCTTGGAAACCTTCACTTCAGCTTCACAGTGTGCCCTTCAAGCTGCTGCAAGAACAA	82
Db	727	CCCTTGGGAAACCTTCACTTCACAGTGTGCCCTTCAAGCTGCTGCAAGAACAA	78
QY	824	CTTAACTGGGATTTGAAGAAACACACTGTGGGACCAATTGGAAACTGGTCAATCTCCAGAAC	88
Db	787	CTTAACTGGGATTTGAAGAAACACACTGTGGGACCAATTGGAAACTGGTCAATCTCCAGAAC	84
QY	884	AACCTGTCAAGTATTCAGTGTGAGCCTTATACGACCAAGATTTGGGGATCATGAATG	94
Db	847	AACCTGTCAAGTATTCAGTGTGAGCCTTATACGACCAAGATTTGGGGATCATGAATG	90
QY	944	TAGCCATCCCCGGGACACTTCACTTTACTCTGCATGTACTCTTATCTCTCAAGAG	100
Db	907	TAGCCATCCCCGGGACACTTCACTTTACTCTGCATGTACTCTTATCTCTCAAGAG	96
QY	1004	AACGTGATTAATTGGGAAGAAAGAAACCATTTGTGATCATCTGSAATCTGTCTCAAAATCC	106
Db	967	AACGTGATTAATTGGGAAGAAAGAAACCATTTGTGATCATCTGSAATCTGTCTCAAAATCC	102
QY	1064	TAGTCCAAATATGCTAAAAAATTTGGACAAAGTTCTCAATGATTTAAGAGGGTATTATTA	112
Db	1027	TAGTCCAAATATGCTAAAAAATTTGGACAAAGTTCTCAATGATTTAAGAGGGTATTATTA	108
QY	1124	CCCCCTTCAATTCAGTGTGACATCATATGTTACTGCAATCTGGGTGGCATTTATCAT	118
Db	1087	CCCCCTTCAATTCAGTGTGACATCATATGTTACTGCAATCTGGGTGGCATTTATCAT	114

QY	1184	TTCTCTGGCAAGGAGATTAAAAAAGGCAAGAAATCCAGAGAAAGTATGAAATGACCCTA	12433
Db	1147	TTGGCTGGCAAGGAGATTAAAAAAGGCAAGAAATCCAGAGAAAGTATGAAATGACCCTA	1206
QY	1244	TTAATATGCCCTTGGTGAAGAAATTCCTGGAAATCTATAAATCATGAGATCCCTTAA	13030
Db	1207	TTAAATGCCCCCTTGGTGAAGAAATTCCTGGAAATCTATAAATCATGAGATCCCTTAA	1266
QY	1304	TCCTTCATGAAGACGTTTGTGTGGTGGACCTCTACGTCAAAAGTGAAGTGTG - TTCC	1362
Db	1267	TCCTTCATGAAGACGTTTGTGTGGTGGACCTCTACGTCAAAAGTGAAGTGTGTTC	1366
QY	1363	TTTCAGTGCATCTGGGAAGATTTCTACCCGACCAACAGTTCTTTCAGCTTCCATTTCCGCC	14222
Db	1327	TTTCAGTGCATCTGGGAAGATTTCTACCTGACCCACAGTTCTTTCAGCTTCCATTTCCACC	1386
QY	1423	CTCATTTATCCCTCAACCCGACCCGACAGGTTTATATACCTCAGCTTTTGTCTTT	1482
Db	1387	CTCATTTATCCCTCAACCCGACCCGACAGGTTTATATACCTCAGCTTTTGTCTTTT	1446
QY	1483	CTGAGGAGAAACAAATATAGACCAT - AAGGGAAGATTTATGATGTGAATATTAAGATGCT	1541
Db	1447	CTGAGGAGAAACAAATATAGACCATTAAGGGAAGATTTATGTAATATTAAGATGCT	1506
QY	1542	GACTTTGCTCTTTCTTGACCTCTTGTTTTCAGTTCAATTTCACTGCTGTACTTTGATGACAG	1601
Db	1507	GACTTTGCTCTTTCTTGACCTCTTGTTTTCAGTTCAATTTCACTGCTGTACTTTGATGACAG	1566
QY	1602	ACACTCTAAATGAAGGCAAAATTCATCATATGTGAATATGAGCTCAGTTTCTTGCA	1661
Db	1567	ACACTCTAAATGAAGGCAAAATTCATCATATGTGAATATGAGCTCAGTTTCTTGCA	1626
QY	1662	GATCAAAATTCACGCTCTCTTCTGTACTGTGAGAGTACACTCTTAATGAAGTTCAAA	1721
Db	1627	GATCAAAATTCGCGTGCTCTTCTGTATAC - GTGAGAGTACACTCT - - - - ATGAAGTCAA	1680
QY	1722	AAGTCTACGCTCTCTCTTCTTAACTCAGTGAAGTAAATGGGCTGCTCAAGTTGA	1781
Db	1681	AAGTCTACGCTCTCTCTTCTTAACTCAGTGAAGTAAATGGGCTGCTCAAGTTGA	1740
QY	1782	AAGAGTCTCTATTTGCACTGTAGGCTGGCGCTGTGTAATGTGACCATCTATTACGTG	1841
Db	1741	AAGAGTCTCTATTTGCACTGTAGGCTGGCGCTGTGTAATGTGACCATCTATTAACTG	1800
QY	1842	CTTGAGGCTGCCACCTCTTTCAGCCACCTGCTTTTCAGTTGGTACCTCCACACC	1901
Db	1801	CTTGA - GCTGCCACCTTTTTCAGCCACCTCTTTTTCAGTTGGTACCTCCACACC	1859
QY	1902	TAGCAATCTCATGACTGGCAAGCAAAAGAGAGAGAGAAATAGCTGCGCGGTCTTTT	1961
Db	1860	TAGCAATCTCATGAGTGGCAAGCAAAAGAGAGAGAGAAATAGCTGCGCGGTCTTTT	1919
QY	1962	AGTTTGGGGGTTTGTGCTTTCTTTTATGAGACCCATTCATTTTCTTATAGTCAATGT	2021
Db	1920	AGTTTGGGGGTTTGTGCTTTCTTTTATGAGACCCATTCATTTTCTTATAGTCAATGT	1979
QY	2022	TTCTTTATACAGATATATTAAGTAAAGAAATCATCAATATGCTAGCTGAAGTGA	2081
Db	1980	TTCTTTATACAGATATATTAAGTAAAGAAATCATCAATATGCTAGCTGAAGTGA	2039
QY	2082	TCCTTTGATGATCATATGAAAGATTAAAAACAGAGTGAAGAAATTCCTTGATTCACAATGA	2141
Db	2040	TCCTTTGATGATCATATGAAAGATTAAAAACAGAGTGAAGAAATTCCTTGATTCACAATGA	2099
QY	2142	AATGCTCTCTTTTCCCTGGCCCCAGAACTTTTATCCACTTACATGATCTACATATTC	2201
Db	2100	AATGCTCTCTTTTCCCTGGCCCCAGAACTTTTATCCACTTACATGATCTACATATTC	2159
QY	2202	TTTAAATTTGATCTGAGGCTCCCTCAACCCAC	2235
Db	2160	TTTAAATTTGATCTGAGGCTCCCTCAACCCAC	2193

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Db	727	CCCTTTGGGAAACCTTCAACTCTCAACTCACAGTGTGCTTCAGCTGCTCTGAAAGAACAA	786
QY	824	CTTAACGTGGGATTGAGAAACCACTGTGTGAGCAATTTGGAAACGTGTCATCTCCAGACC	883
Db	787	CTTAACGTGGGATTGAGAAACCACTGTGTGAGCAATTTGGAAACGTGTCATCTCCAGACC	846
QY	884	AACCTGTCAAGTCAATTCAGTGTGAGCTCTCATCAGCACACAGATTTTGGGATTCATGAAC	943
Db	847	AACCTGTCAAGTCAATTCAGTGTGAGCTCTCATCAGCACACAGATTTTGGGATTCATGAAC	906
QY	944	TAGCATCCCTCGGACCGAGCTGACGTTTAACTCGTGCATGTACCTTCATCTGTCTCAAGAG	1007
Db	907	TAGCATCCCTCGGACCGAGCTGACGTTTAACTCGTGCATGTACCTTCATCTGTCTCAAGAG	966
QY	1004	AACCTAGTTAATTGGGAGAGAAAGAACCAATTTGTGAATCATCTGTGAATCGTGAACATCC	1066
Db	967	AACCTAGTTAATTGGGAGAGAAAGAACCAATTTGTGAATCATCTGTGAATCGTGAACATCC	1022
QY	1064	TAGTCCAAATATGTGCAAAATTTGGACAAAAGTTTCTCATATGTTTAAAGAGGGTCAATTAA	1122
Db	1027	TAGTCCAAATATGTGCAAAATTTGGACAAAAGTTTCTCATATGTTTAAAGAGGGTCAATTAA	1086
QY	1124	CCCCCTTCATTCAGTGTGAGTGCATGTGATCTGATCTGCTGGGTGGCAATTAATCT	1188
Db	1087	CCCCCTTCATTCAGTGTGAGTGCATGTGATCTGATCTGCTGGGTGGCAATTAATCT	1144
QY	1184	TTGGCTGGGACAAAGACATTTAAAAAAGGCACAGAAATCCACAGAGATGATGAATGACCATA	1243
Db	1147	TTGGCTGGGACAAAGACATTTAAAAAAGGCACAGAAATCCACAGAGATGATGAATGACCATA	1206
QY	1244	TTTAAATCGCCCTTGGTGAAGAAATAATCTTGGAATACTTAAATTCATGATGATCCCTTAA	1303
Db	1207	TTTAAATCGCCCTTGGTGAAGAAATAATCTTGGAATACTTAAATTCATGATGATCCCTTAA	1266
QY	1304	TCCTTCATGAAACGTTTGTGTGTGTGCACTCTCTACGTCAACATGTAAGTGTG - TTC	1362
Db	1267	TCCTTCATGAAACGTTTGTGTGTGTGCACTCTCTACGTCAACATGTAAGTGTGTGTC - TC	1326
QY	1363	TTTCAGTGCATCTGGGAGAAATTTTACCCGACCAACAGTTCCTTCAGCTCCATTTCCGCC	1422
Db	1327	TTTCAGTGCATCTGGGAGAAATTTTACCTGTGACCAACAGTTCCTTCAGCTCCATTTCCGCC	1386
QY	1423	CTCATTTTATCCCTCACACCCCGACCCACAGGTGTTTATACAGCTCAGCTTTTGTCTTTT	1482
Db	1387	CTCATTTTATCCCTCACACCCCGACCCACAGGTGTTTATACAGCTCAGCTTTTGTCTTTT	1446
QY	1483	CTGAGAGAAACAAATATAGACCAT - AAGGGAAGGATTTATGTGGAATATATAAGTGGCT	1541
Db	1447	CTGAGAGAAACAAATATAGACCATATAAGGGAAGGATTTATGTGGAATATATAAGTGGCT	1506
QY	1542	GACTTTGTCTTTCTTGACCTTTGTTTACGTTTCATTCAGTGTGATCTGATGTAGACAG	1601
Db	1507	GACTTTGTCTTTCTTGACCTTTGTTTACGTTTTCAGTTCAATTCAGTGTGATGTAGACAG	1566
QY	1602	ACACTTCAATATGAGCAAAATTTATATACATATATGTAATATGACCTCAGTTTTCTTGCA	1661
Db	1567	ACACTTCAATATGAGCAAAATTTATATACATATATGTAATATGACCTCAGTTTTCTTGCA	1626
QY	1662	GATCAAAATTCACCTGCTCTCTGTATATCTGTGAGAGTCACTCTTATAGAAAGTTCAAA	1721
Db	1627	GATCAAAATTCACCTGCTCTCTGTATATCTGTGAGAGTCACTCTTATAGAAAGTTCAAA	1680
QY	1722	AAGTCTACGCTCTCTTTCTTTCTAACCTCAGTGAAGTAATGGGGTCTGTCAAGTTGA	1781
Db	1681	AAGTCTACGCTCTCTTTCTTTCTAACCTCAGTGAAGTAATGGGGTCTGTCAAGTTGA	1740
QY	1782	AAGAGTCTTATTTGCACTGAGAGCTGCGGCTGTGGAATTTGGACATTCATTAATCTGG	1841
Db	1741	AAGAGTCTTATTTGCACTGAGAGCTGCGGCTGTGGAATTTGGACATTCATTAATCTGG	1800

OY	1842	CTTGAGGCGCTCCGCCACCTTCTTCAGCGCACCTCCTTTTCAAGTTGGCTGCATTCACAACC	1901
Db	1801	CTTCA-GCGCTCCCCACCTCTTTCAGCGCACCTCCTTTTCAAGTTGGCTGCATTCACAACC	1859
OY	1902	TAGCATCTCATFAGNRSCCAAGAAMAAGSGAACAAGAAATTAACCTCCGCGGTATTTTT	1961
Db	1860	TAGCATCTCATFAGNRSCCAAGAAMAAGSGAACAAGAAATTAACCTCCGCGGTATTTTT	1919
OY	1962	ACTTTGGGGGTTTGGCTGTTTCCTTTTATGAGACCCATTTCCTTAATTAAGTCAATGT	2021
Db	1920	AATTGGGGGGTTTGGCTGTTTCCTTTTATGAGACCCATTTCCTTAATTAAGTCAATGT	1979
OY	2022	TTCCTTTATCAGCATATATTAGTAGAAAACATACATAAGTAATGTACTGCAAGTGA	2081
Db	1980	TTCCTTTATCAGCATATATTAGTAGAAAACATACATAAGTAATGTACTGCAAGTGA	2039
OY	2082	TCTCTTTATGTCATATGGAAGAGAGTTAAACAGGTGAGAATTCCTTGATTCAACATGA	2141
Db	2040	TCTCTTTATGTCATATGGAAGAGAGTTAAACAGGTGAGAATTCCTTGATTCAACATGA	2099
OY	2142	AATGCTCCTCTTCCCCHGCCGCCAGAACCTTTATCCACTTACTAGATTCTACATAATC	2201
Db	2100	AATGCTCCTCTTCCCCHGCCGCCAGAACCTTTATCCACTTACTAGATTCTACATAATC	2159
OY	2202	TTTAATTTTCATCTCAGGSCCTCCCTCAACCCCAAC	2235
Db	2160	TTTAATTTTCATCTCAGGSCCTCCCTCAACCCCAAC	2193
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LOCUS	DEFINITION	Sequence 1 from patent US 5679346.	
ACCESSION	I70140		
VERSION	I70140.1	GI:3006275	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 2330)		
TITLE	Tedder,R.F. and Spertini,O.G.		
JOURNAL	Methods of blocking adhesion with anti-Iam1-3 antibody Patent: US 5679346-A 1 21-OCT-1997;		
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Best Local Similarity	98.5%;	Pred. No. 0;	
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OY	104	AANTAGAGAAGGACCAAGCAAAGCCATTCATTTCCATGAAATSTCAGAGCACCAGAG.	163
Db	67	AANTAGAGAAGGACCAAGCAAAGCCATTCATTTCCATGAAATSTCAGAGCACCAGAG	126
OY	164	GGACTATATGGAACATCTTCAAGTGTGGGGGGGAGCAANTGCTGTGTGATTTCTGGC	223
Db	127	GGACTATATGGAACATCTTCAAGTGTGGGGGGGAGCAANTGCTGTGTGATTTCTGGC	186
OY	224	ACATCATGGAACCTTACTGCTGACTTACCATTAATTCATAAAAAACCATGGAACGCAAG	283
Db	187	ACATCATGGAACCGGACTGCTGACTTACCATTAATTCATAAAAAACCATGGAACGCAAG	246
OY	284	GCGTGAAGATTCGCCGAGCAATTTACACAGATTTAGTTGCCATCAAAAACAAGCGGA	343
Db	247	GCGTGAAGATTTGCCGAGCAATTTACACAGATTTAGTTGCCATCAAAAACAAGCGGA	306

QY	344	AATTGAGTATCTGGAGAAACATCTGCGCTTCACTGCTTCTTACTGATAGAAATCGG	403
Db	307	AATTGAGTATCTGGAGAAACATCTGCGCTTCACTGCTTCTTACTGATAGAAATCGG	366
QY	404	GAAGATAGGAGAAATTTGGACGTGGGGTGGGAACCAACAATCTCTCACTGAAGACAGA	463
Db	367	GAAGATAGGAGAAATTTGGACGTGGGGTGGGAACCAACAATCTCTCACTGAAGACAGA	426
QY	464	GAACGTGGGAGATGGTGGAGCCCAACAAGAAAGACAGAGAGCTGGTGGAGATCTA	523
Db	427	GAACGTGGGAGATGGTGGAGCCCAACAAGAAAGACAGAGAGCTGGTGGAGATCTA	486
QY	524	TATCAAGAAACAAAGATGACAGGCAATGGAACGATGACGCTGCCACAACCTAAGGC	583
Db	487	TATCAAGAAACAAAGATGACAGGCAAAATGGAACGATGACGCTGCCACAACCTAAGGC	546
QY	584	AGCCCTCTGTTACACAGCTTCTTGGCAGCGCTGGTCATGAGTGGGCATGGAATGTG	643
Db	547	AGCCCTCTGTTACACAGCTTCTTGGCAGCGCTGGTCATGAGTGGGCATGGAATGTG	606
QY	644	AGAAATCATCAATTAATCACACCGTCGACACTGTGATGCGGTACTATGCGCCCAAGTCTCA	703
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QY	704	GCTTGTGATTCAGTGTGAGCCTTTGGAGGCCCAAGAGCTGGTACCATGAGATCTGACTCA	763
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QY	2022	TTCTTTTATCAGATTAATTTAGTAAGAAAACATCACATGAAATGCTAGCTGCAAGTGA	2081
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Db	2100	AATGCTCTCTCTTCCCTGGCCCGCAGAACTTTTTCACATTAAGTCTAATCTACATATTC	2159
QY	2202	TTTAAATTTTCATGCTCAGAGCCTTCCCTCAACCCAC	2235
Db	2160	TTTAAATTTTCATGCTCAGAGCCTTCCCTCAACCCAC	2193

RESULT	10
HS246000	
LOCUS	HS246000 1569 bp mRNA PRI 08-SEP-1999
DEFINITION	Homo sapiens mRNA for leucocyte adhesion receptor, L-selectin.
ACCESSION	AJ246000
VERSION	AJ246000.1 GI:5852071
KEYWORDS	L-selectin gene; Leucocyte adhesion receptor.
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
Eutheria; Primates; Catarrhini; Homiidae; Homo.	
REFERENCE	1 (bases 1 to 1569)
AUTHORS	Fieger,C.B.
JOURNAL	Thesis (1998) Freie Universitaet Berlin, Fachbereich Chemie
REFERENCE	2 (bases 1 to 1569)
AUTHORS	Fieger,C.B.

TITLE Direct Submission
JOURNAL Submitted (04-SEP-1999) Fieger C.B., Benjamin Franklin Klinikum der
Freien Universitaet Berlin, Institut fuer Klinische Chemie &
Pathobiochemie, Hindenburgdamm 30, 12200 Berlin, GERMANY

FEATURES

location/Qualifiers
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414 GGAATATGAGCGTGGGGGAGACCAACAAATCTCTCACTGAAGACAGAGAACTGGGGA 473
361 GGAATATGAGCGTGGGGGAGACCAACAAATCTCTCACTGAAGACAGAGAACTGGGGA 420

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LOCUS Papio hamadryas anubis L-selectin precursor mRNA, complete cds.
DEFINITION U52074
ACCESSION U52074
VERSION U52074.1 GI:1326148
KEYWORDS
SOURCE olive baboon.
ORGANISM Papio hamadryas anubis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Papio.
REFERENCE 1 (bases 1 to 1510)
Tsurushita, N., Fu, H. and Berg, E.L.
AUTHORS PCR cloning of the cDNA encoding baboon L-selectin
TITLE Gene 181 (1-2), 219-220 (1996)
JOURNAL MEDLINE 97128794
REFERENCE 2 (bases 1 to 1510)
Tsurushita, N.
AUTHORS Direct Submission
TITLE Submitted (21-MAR-1996) Noya Tsurushita, Protein Design Labs,
JOURNAL Inc., 2375 Garcia Avenue, Mountain View, CA 94043, USA
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DEFINITION Pan troglodytes L-selectin mRNA, complete cds.
ACCESSION U73728
VERSION 073728.1 GI:1658019
KEYWORDS
SOURCE chimpanzee.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
REFERENCE 1 (bases 1 to 1119)
AUTHORS Budman,J.I., Fu,H., Johnson,C.E., Thakur,A.B., Berg,E.L. and
Tsurushita,N.
TITLE Cloning of the cDNA encoding L-selectin from nonhuman primates
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1119)
AUTHORS Budman,J.I., Fu,H., Johnson,C.E., Thakur,A.B., Berg,E.L. and
Tsurushita,N.
TITLE Direct Submission
JOURNAL Submitted (08-OCT-1996) Protein Design Labs, Inc., 2375 Garcia
Avenue, Mountain View, CA 94043, USA
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ORIGIN

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Db 61 TGGGGGTGACAAATGCTGTGATTTCTGCTGACATCATGGAACCTGCTGACT 120
OY 249 TACCATTAATCTGAAAAACCATGCAAAAGGCTGAGAGATTCGCCAGACAAT 308
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Db 121 TACCATTAATCTGAAAAACCATGCAAAAGGCTGAGAGATTCGCCAGACAAT 180
OY 309 TACACAGATTAGTTGCCATACAAACAAAGCGGAATTTAGTATCTGGAGAACTCTG 368
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Db 181 TACACAGATTAGTTGCCATACAAACAAAGCGGAATTTAGTATCTGGAGAACTCTG 240
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Db 361 AACCAAGAACCAAGAGAGACTGCTGAGATCTATATCAAGAGAAACAAAGATGACGAC 420
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Db 1081 GGCACAGAAATCCAGAGAGATGATGAATGACCCATATTA 1119
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LOCUS PP073729 1119 bp mRNA PRI 05-NOV-1996
DEFINITION Pongo pygmaeus L-selectin mRNA, complete cds.
ACCESSION U73729
VERSION 073729.1 GI:1658017
KEYWORDS
SOURCE orangutan.
ORGANISM Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pongo.
REFERENCE 1 (bases 1 to 1119)
AUTHORS Budman,J.I., Fu,H., Johnson,C.E., Thakur,A.B., Berg,E.L. and

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
FEATURES
SOURCE
CDS
BASE COUNT
ORIGIN
Query Match
Best Local Similarity
Matches 1098; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
48.0%; Score 1085.4; DB 85; Length 1119;
98.1%; Pred. No. 5.2e-281;
233 c 273 g 277 t

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MMU73730
LOCUS MMU73730 1119 bp mRNA PRI 05-NOV-1996
DEFINITION Macaca mulatta L-selectin mRNA, complete cds.
ACCESSION U73730
VERSION U73730.1 GI:1658015
KEYWORDS
SOURCE
ORGANISM
Macaca mulatta.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecidae; Macaca.
REFERENCE
AUTHORS
Budman, J. I., Fu, H., Johnson, C. E., Thakur, A. B., Berg, E. L. and
Tsurushita, N.
TITLE
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REFERENCE
AUTHORS
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Db 529 GGAGGACGCGTGGAGATCTATATTCAGAGAAAGGCTCAGAGAGCTGGGAAAAATGGAAGATGA 588
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Search completed: January 12, 2001, 21:39:01
Job time: 18955 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2001, 20:00:14 : Search time 125.58 Seconds
(without alignments)
6757.621 Million cell updates/sec

Title: US-09-119-209-1

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Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	2255.8	99.9	2259	16	092802 Human LHR CDNA. H
4	2255.8	99.9	2259	16	T00869 Human LHR CDNA. H
5	2255.8	99.9	2259	17	T30003 Human lymphocyte c
6	2255.8	99.9	2259	19	V19012 Homo sapiens lymph
7	2254.2	99.8	2259	14	043154 Human lymphocyte h
8	2251.8	99.7	2259	12	012118 Sequence encoding
9	2241.6	99.2	2260	13	023623 Human lymphocyte h
10	2241.2	99.2	2262	13	024987 Sequence encoding
11	2127.8	94.2	2350	17	T14723 Human Leu8 antigen
12	2126.2	94.1	2350	13	021184 Encodes T lymphocy

13	2126.2	94.1	2350	19	V63460 Human Leu8 antigen
14	2126.2	94.1	2350	20	V81217 Human Leu8 antigen
15	2087.6	92.4	2330	15	071006 l-selectin cDNA. c
16	2086	92.3	2330	14	035142 LAM-1 B125 cDNA. c
17	2076.4	91.9	2330	14	038839 Sequence of LAM-1
18	2076.4	91.9	2330	18	T72270 Human lymphocyte-a
19	2074.8	91.8	2330	14	037304 LAM-1 cDNA from pl
20	2058.8	91.1	2327	11	005871 Sequence encoding
21	2033.4	90.0	2330	13	031767 Human LAM-1. Homo
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24	970.2	42.9	141589	21	A35005 Human adenosine re
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26	922.2	40.8	1696	15	071015 Lym-1 gene exon X
27	856.8	37.9	2214	13	023624 Murine lymphocyte
28	856.8	37.9	2214	13	024888 Sequence encoding
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36	828.8	36.7	1496	11	005542 Mus musculus lymph
37	817.8	36.2	2219	19	V19013 Lym-1 gene exon I
38	385.2	17.1	5866	15	038840 Sequence of exons
39	385.2	17.1	5866	13	031768 Genomic Human LAM-
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ALIGNMENTS

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AC V08321;	
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DT 02-FEB-1999	(first entry)
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DE Human lymphocyte homing receptor coding sequence.	
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KW Lymphocyte homing receptor; LHR; lymphocyte cell-surface glycoprotein;	
KW lymphocyte binding; endothelium; graft rejection; inflammation; therapy;	
KW arthritis; autoimmune disease; lymphoma metastasis;	
KW lymphocyte accumulation; human; ss.	
XX	
OS Homo sapiens.	
XX	
PN US5840844-A.	
PD	
PD 24-NOV-1998.	
XX	
PF 10-AUG-1995;	95US-0513278.
XX	
PR 23-FEB-1989;	89US-0315015.
PR 31-OCT-1991;	91US-0786149.
PR 06-MAY-1993;	93US-0059029.
PR 10-AUG-1995;	95US-0513278.
XX	
PA (GENE) GENENTECH INC.	
PA (REGC) UNIV CALIFORNIA.	
XX	
PL Lasky LA, Rosen SD, Slinger MS, Stachel SE;	
XX	
DR WPI: 1999-034122/03.	
DR P-PSDB; W73264.	

XX Lymphocyte homing receptor polypeptides - useful for inhibiting
PT lymphocyte binding to lymphoid endothelium
XX
PS Disclosure; Fig 1; 33pp; English.
XX
CC This sequence encodes the human lymphocyte homing receptor (LHR) of the
CC invention. LHR is a lymphocyte cell-surface glycoprotein that mediates
CC the binding of lymphocytes to the endothelium of lymphoid tissue. Soluble
CC LHR polypeptides, lacking signal peptide (amino acids 1-36),
CC transmembrane domain (amino acids 333-355) and cytoplasmic domain (amino
CC acids 356-372), can be used therapeutically to compete with the normal
CC binding of lymphocytes to lymphoid tissue and are especially useful for
CC organ or graft rejection treatment protocols, for treating inflammations
CC such as arthritis and other autoimmune diseases, for control of lymphoma
CC metastasis and for treating conditions involving lymphocyte accumulation.
CC LHR polypeptides can also be used in assays for LHR, anti-LHR antibodies
CC or competitive inhibitors of LHR activity, and for purifying anti-LHR
CC antibodies, and as immunogens for raising anti-LHR antibodies.
XX
SQ Sequence 2259 BP; 635 A; 517 C; 488 G; 619 T; 0 other:

Query Match 100.0%; Score 2259; DB 20; Length 2259;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 241 gctgacttaccatttattctgaaaacccatgacctgcaaaaggctgagaaattc 300
QY 301 GAGACAAATTACAGATTAGTTCCTATACAAACAAGGCGAATGATGATCTGGAGA 360
DB 301 gagacaattacagatttagttcctatacaaacaaggcggaattgatatctggaga 360
QY 361 AGACTGTGCCCTTCAGTCGTTCTTACTACTGATAGAGATCCGGAAGATGAGGAATAT 420
DB 361 agactgtgcccttcagtcggttcttactactgataagaaaggaacttggagatata 420
QY 421 GGAGCTGGTGGGAACCAAAATCTCTCACTGAAGAGAGAGACTGGGGAGATGGTG 480
DB 421 ggagctgggtgggaaccaaactctctcactgaagagaggaacttggggagatgg 480
QY 481 AGCCCAACAACAAGAGAGACAGAGAGACTGCTGAGATCTTATCAAGAGAAACAAG 540
DB 481 agcccaacaacaagagagagagagactgctgagatcttatacaagagaaacaag 540
QY 541 ATGCAGCAATGGAAGATGACGCTGCACAACTAAAGGAGCGCTCTGTTCACAG 600
DB 541 atgcagcaatggaaagatgacgctgcacaaactaaaggagcgctctgttcacag 600
QY 601 CTTCCTTGCAAGCCCTGTCATGCAAGTGGCCATGAGAAATGATCAATCAATTAATC 660
DB 601 ctctcttgcaagccctgtcatgcaagtggccatgagaaatgataatcaatcaat 660
QY 661 ACACCTGCAACGTGTATGTGGGTACTATAGGCCCCAGTGTGATTCAGTGTG 720
DB 661 acacctgcaacgtgtatgtgggtactatagggccccaagtgtgatttcagtgtg 720

DB 661 acacctgcaacttgatgtg99gtactatg99cccaagtgctgacttgatcagtg 720
QY 721 AGCCTTGGAGCCCCACAGCTGGTACATGACTGACTACACCCCTTTGGAAACTTCA 780
DB 721 agccttggagcccccacagctgggtacatgactgactacaccccttggaaacttca 780
QY 781 GCTTCAGCTCAGTGTGCTTCCAGCTGCTCTGAAGAACAACTTATACGTGGATGAG 840
DB 781 gcttcagctcagtggtgcttccagctgctctgaagaaacttattacgtggatgag 840
QY 841 AAACACCTGTGGACCATTTTGGAACTGTGATCTCCAGAACCAACCTGTCAAGTATTC 900
DB 841 aaacacctgtggaccattttggaaactgtgatctccagaaacacacttaacggtat 900
QY 901 AGTGTAGCCCTCTATGACGACAGATTTGGGGATGATGAACCTGATACCATCCCTGGCA 960
DB 901 agtgtagccctctatgacgacagatttggggatgatgaacctgataccatccctgg 960
QY 961 GCTTCAGCTTACCTGTGATGATGATCTTCACTGCTCAGAGAGACTGATTAATTGGGA 1020
DB 961 gcttcagcttacctgtgcatgatacttcaactctgctcagaggaactgtaattgga 1020
QY 1021 AGAAGAAACCATTTTGTGAATCATCTGGAATCTGGCAATCTCTACTCCATATGTCAA 1080
DB 1021 agaagaaaccattttgtgaatcatctggaaatctggcaatctctactccatattgt 1080
QY 1081 AATTGGCAAAAGTTCATGATTTAAGAGAGGTGATTAACCCCTTCATTTCAG 1140
DB 1081 aattggcaaaagtctcatgatttaagagaggtgatttaaccccttcatttcag 1140
QY 1141 TGGCAGTCATGTTACTGATCTCTGSGTGTGGCATTTATCTTTGGCTGGCAAGAGAT 1200
DB 1141 tggcagtcattgttactgatctctgsgtgtggcatttatctttggctggcaagat 1200
QY 1201 TAAAAAAGCCAGAAATCCAGAGAGATGATGAACCATATTAATCGCCCTGGTG 1260
DB 1201 taaaaaagccagaatccagagagatgatgaacctatataatcgccctggtg 1260
QY 1261 AAAGAAATTTTGGGATCTTAAATATCATGATCTTTAAATCCTTCAATGAACGTT 1320
DB 1261 aaagaaattttgggattttaaatacatgatcttttaaatccttcaatgaacgtt 1320
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DB 1321 ttgtgtgtgggacctccagctcaacatgagtgtcttccatgagcatctgggaag 1380
QY 1381 ATTTCTACCCGACCAAGTTCCTTACGCTTCCATTTCCGCCCTCATTTATCCCTCAAC 1440
DB 1381 atttctacccgaccaaagttccttaccgcttccatttccgccctcatattccctca 1440
QY 1441 CCCAGCCCAAGGTGTATATACGCTGAGCTTTTGTCTTTTCTGAGAGAAACAATAA 1500
DB 1441 cccagcccaaggtgtatatacagctgttcttcttcttcttcttcttcttcttctt 1500
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DB 1501 gaccataaaggaaagattcatgtggaatatagaataggctgacttggctttcttggac 1560
QY 1561 TCTTGTTTTCAGTTCAATTAAGTGTGATCTGATGACAGACACTTCAATGAAGTGC 1620
DB 1561 tcttgttttcagtttcaatttaagtgtgatctgatacagacacttcaatgaagtgc 1620
QY 1621 AAATTTGATACATATGGAATATGAGTACTGATTTTCTTGAGATGCAAAATTTACGTCGTC 1680
DB 1621 aaatttgatatacatatggaaatatagactgatttcttcttcttcttcttcttcttct 1680
QY 1681 TTCTGTATCTGTTGAGAGTACACTTATAGAAAGTTCAAAAAGTTAGCTCTCTCTTC 1740
DB 1681 ttctgtatctgttgagagtacacttataagaaagttcaaaaagttagctctctcttc 1740
QY 1741 TTCTTAACCTCAGGAAGTATGGGTCCTGCTCAAGTTTGAAGAGCTCTATTTGCACATG 1800
DB 1741 ttcttaacctcaggaagtatgggtccctgctcaagtttgaagagctctatttgcacatg 1800

OY	1801	TAGCGTCGCGGTGTCGAATTGGACCATGCTATTATTAACGTGCGTTGAGCGCTCCACGCT	1860
Db	1801	taagcttcgcgcgtcgtgaaatttgagacacatccatttaaaccggtctcagacctcccaactt	1860
OY	1861	CTTTCAGCGACGCTCTCTTTTTCAGTTTGGGCTTCATTCCACACGCTACGATCTGCATGAGTGGCA	1920
Db	1861	cttcagcgacacctctctcttcttcagtttgctgactctccaaacctgactctcatgagtgca	1920
OY	1921	AGCAAAAGGAGAGAGAGAGAAATAGCGTCGCGGGTTTTTATGTTTGGGGGTTTTGCTGT	1980
Db	1921	agcaaaagagagagagagagaaataagcctgcgaggttctttagtcttgaggggttcttcgcgt	1980
OY	1981	TTCCTTTTATGACAGACCCGATTCCTATTGCTTATGCTTAATGCTTTCCTTTATCAGATATTAA	2040
Db	1981	tctctctttagagagcccatctccattctctatagtaagtaagttctcttctatccagatata	2040
OY	2041	TTATGTAAGAAAAATCATCTGAATGCTAGCTGCAAGTGACATCTCTTTGATGTCTATATGG	2100
Db	2041	ttagtaagaaaaacatccacttgaaatgctagctgagaaatgagacatctctttagatgatactg	2100
OY	2101	AAGGTTAAAAAGGTGAGAAATTCCTTGATTCACAAATGAATAGTCTCTCTTCCCGCTG	2160
Db	2101	aaaggtctaaacaagtgagaaatactctctgattccacaagaagatgcctccctctccctg	2160
OY	2161	CCCCAGAACTTTTATGCGACTTACCTAGATTCTACATATTCTTTAAATTTCATCTCAGGC	2220
Db	2161	ccccagaaactttatctcaacttaccctagatcttcaaatcttctttaaattcaatcttcagcg	2220
OY	2221	CTTCCCTCAACCCCGAGGGGCGGCACACACATCGAATTTC	2259
Db	2221	cttccctcaaaccccgagggcgccgacagaaacttgaatttc	2259

RESULT	2	
044243		
1D	Q44243	standard; DNA; 2259 BP.
XX		
AC	Q44243;	
XX		
DT	11-JAN-1994	(first entry)
XX		
DE	HuLHR DNA.	
XX		
KW	Human; murine; lymphocyte; cell surface glycoprotein; homing receptor;	
KW	LHR: endohepatic lymphoid tissue; signal: domain; complement binding;	
KW	carbohydrate binding; epidermal growth factor-like; egf; intracellular	
KW	transmembrane binding; cytoplasmic; ligand binding partner protein;	
KW	TMD; LBPP; ss.	
XX		
OS	Homo sapiens.	
XX		
EH	Key	Location/Qualifiers
FT	CDS	129..1247
FT		/*tag= a
FT	sig_peptide	186..224
FT		/*tag= b
FT	mat_peptide	243..1244
FT		/*tag= C
XX		
PN	US5225538-A.	
XX		
PD	06-JUL-1993.	
XX		
PE	23-FEB-1989;	89US-0315015.
XX		
PR	23-FEB-1989;	89US-0315015.
PR	22-NOV-1989;	89US-0440625.
PR	16-DEC-1991;	91US-0808122.
XX		
PA	(GETH) GENENTECH INC.	
XX		
1I	Capon DJ, Lasky LA;	

XX WPI: 1993-226664/28.
DR P-PSDB: R38908.
XX
PT New lymphocyte homing receptor immunoglobulin fusion
PT polypeptide(s) - used to inhibit binding of lymphocytes in
PT therapeutic and diagnostic uses
XX
XX
XX Disclosure; Fig 1: 44pp; English.
PS
XX The sequences given in Q44243-44 encode human and murine lymphocyte
CC cell surface glycoprotein (LHR) respectively. The proteins encoded
CC by these sequences mediate the binding of lymphocytes to the
CC endothelium of lymphoid tissue. LHR is a glycoprotein which contains
CC a signal domain, a carbohydrate binding domain, an epidermal growth
CC factor-like (egf) domain, at least one complement binding domain
CC repeat, a transmembrane binding domain (TMD) and a charged intra-
CC cellular or cytoplasmic domain. The murine and human amino acid
CC sequences show a high degree of overall homology (83%), however
CC degrees of homology between the various domains is variable. These
CC proteins may be fused to a ligand binding partner protein (LBP) which
CC causes an increase in the half life of the LHR. The fusions may be
CC used therapeutically to compete with the normal binding of
CC lymphocytes to lymphoid tissue. They may be used in organ or graft
CC rejection and for the treatment of inflammation.
XX
XX Sequence 2259 BP; 635 A; 516 C; 489 G; 619 T; 0 other;

Query Match	99.98	Score 2255.8	DB 14	Length 2259
Best Local Similarity	99.98	Pred. No. 0		
Matches 2257	Conservative	0	Mismatches 2	Indels 0
				Gaps 0

QY	1	GATTTCAGGTGTGCGTGGCTTCCCTACCGGACGACGACACACATCCCTTTGGCAAGACCT	60
Db	1	gaattcccaagtgtctgtgtcttccctccacgtgacgcagcaacatctcttttggcaagacct	60
QY	61	GAGACCCCTTTTGCTTAAGTCAAGACGCGTCAATAGCGCTCCAGAACAACTAGAGAAAGACCA	120
Db	61	gagaccccttggctcaagtccaagaggtcccaatgggtcttgagaaagaaactcagagaagaccaa	120
QY	121	GCAAGCCCATGATATATTTCCATGGAATGTCAAGACACCCAGAGGACTTATGCAACATCT	180
Db	121	gcaagcccatgatatttccatggaatgtcagacaccagaggaacttatggaacatc	180
QY	181	TCAAGTTGTGGGGGTGGACATGCTCTGTGTGTGATTTTCCTGGCAGATCATGGAACCTACT	240
Db	181	tcaagttgtgggggtggacaatgctctgtgtgtatttccctggcacatcagaaactact	240
QY	241	GCTGGACTTACCATTTATTTCTGAAAAACCCATGAATGCGCAAGGCGCTAGAAATTTCTGCC	300
Db	241	gctggacttacccatttcttctgaaaaaccatgaaacttgcgaagaggtccatgaagattctgcc	300
QY	301	GAGACAATTACACAGATTTTAGTTGGCATATACAAAACAAGCGCGAAATTTGACTATTCTGGAGA	360
Db	301	gagacaattacacagattttagttgcatacaaaaacaagcggaatttgattctcggaga	360
QY	361	AGACTGTGCCCTTCAATGTCGTTCTTACTACTACGATNGGAATTCGGAGATATGAGGAGATAT	420
Db	361	agactgtgcccttcaatgtcttcttactactcgtgaataagaaatctcggaaatac	420
QY	421	GCAGCTGGTGTGGACCAACAACAAATCTCTCACTAGCAAGACAGAGAATCTGGCGAGATCGTG	480
Db	421	gcaagtgtgtgggaaaccaacaactctctcactcgaagaagcagagaactctggggagatcgtg	480
QY	481	AGCCCCAACACAGAGAACAAGAGGAGACTTGCCTGGAGATCTTATATTCAGAGAACAAG	540
Db	481	agccccaaacaagaagaacaagagactcgtgagatcttatatacaagagaacaag	540
QY	541	ATGCAAGCAATTGAACAGATGACCCCTGGCCCAACAACTAAAGGCAAGCCCTCTGTTACACAG	600
Db	541	atgcaagcaattggaacagatgacccctggcccaaaactaaagcgagccctctgttacaacag	600

QY 601 CTTCTGCGACCCCTGGTCAATGCAATGAGAGATGTGATGAAATCATCATATATC 660
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 Db 601 ctctctgcagccctcgtctacatgacgtgcctatgagaaatgtctgaaatcatcaataatc 660
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 QY 661 ACACCTCACTGTGATGTGGGGTACTAATGAGGCCCAAGTGTGAGCTTTGTGATTCAGTGTG 720
 |||
 Db 661 acacctgaaactgagatgagtgaggaatgagggcccaagtgctcagcttgatcatcagtg 720
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 QY 721 AGCCTTTGAAGGCCCGACAGCTGGGTACCAATGAGCTGTACTACCCCTTTTGAAGTTTCA 780
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 Db 721 agccttgagggcccgagcgtggtacacatgacgtctacacccctcttgaaacttca 780
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 QY 781 GCTTACGCTACAGTGTGCTTACGCTCTCTAAGAAACAACTTAACTGGGATTTGAAG 840
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 Db 841 aaacacactgtgacacatttgaaactgucattccaaacacactgccaagtatc 900
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 QY 1081 AATTGGACAAAGTTTCTCAATGATTAAGAGAGGATTAATTAACCCCTTTCATTCAG 1140
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 Db 1381 attctacccgacccaacaaagttcctcagctcattcgcgccctcalttaccctaac 1440
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 Db 2221 ctccctcaacccacagggcgccgacgacacatggaattc 2259
 |||

RESULT 3
 ID 092802
 ID 092802 standard; cDNA; 2259 BP.
 AC 092802;
 XX
 DT 01-DEC-1995 (first entry)
 XX
 DE Human LHR cDNA.
 KW Lymphocyte homing receptor; lymphocyte cell surface glycoprotein;
 KW LHR; ligand binding partner; immunoglobulin; constant region;
 KW antibody engineering; immunomodulator; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT CDS 129..1247
 FT Location/Qualifiers
 FT sig_peptide 186..224
 FT mat_peptide 243..1244
 FT /*tag= a
 FT /*tag= b
 FT /*tag= c
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 XX
 PF 23-FEB-1989; 89US-0315015.
 XX
 PR 22-NOV-1989; 89US-0440625.
 PR 23-FEB-1989; 89US-0315015.
 PR 16-DEC-1991; 91US-0808122.
 PR

QY 721 AGCTTTGGAGCCCGACAGCTGGGTACCATGAGCTGACTGACCCCTTTGGAACTTCA 780
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 Db 721 agccttggagggcccccagagctgggtaccagtgactgtaccaccccttggaaacttca 780
 QY 781 GCTTTCAGCTCAGAGTGTGCTTTGACGCTGTCGAAGGAACAACCTTAAGTGGATTGAAG 840
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 Db 781 gcttcagctcacaagtgcttcctcagctcctcgaaggaacaacttaacttgagatcgag 840
 QY 841 AAACACCCTGAGACCAATTTGGAAACGTGTATCTCCAGAACCAACGTCGAAGGATATTC 900
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 841 aaacacccttgagaccaatcttgaaacctcgtaccacccagaacacccgtcgaagtgaatcc 900
 QY 901 AGTGTGACCTCTATTCACAGCACCAGATTTTGGGATCATGAAGTGAAGCCATCCCTGGCCA 960
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 Db 901 agtgtgagccctctacagcaccagatctggggatcatgaactgtgagccatccctggcca 960
 QY 961 GCTTTCAGCTTACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
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 QY 1081 AATTGGACAAAGTTTCTCAATGATTAAGAGGGTGAATTATTAACCCCTCTTCAATTCGAG 1140
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 QY 1141 TGGCAGTCATGCTTACTGATCTCTGCGGTTGGCATTTATCATTTTGGCTGGCAAGGAGAT 1200
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 Db 1261 aaagaaatctcttggaatatacctaaataatcatgagatcccttaactctccatgaaagctt 1320
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 Db 1381 atttctaccgcaacaacagcttccctcagcttccatctcgcctccatcttalcctcccaacc 1440
 QY 1441 CCCAGCCACAGGTGTATATACAGCTCAGCTTTTGTCTTTCTTGTGAGGAGAAACAATTA 1500
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 Db 1501 gaccataagggaaagatcatctgtaaatataaagagcgacgtcttgccttcttgcac 1560
 QY 1561 TCTTGTGTTCAGTTTCATTTACGTGCTGTACTTGTATGACACACACTTTCATATGAAAGTGC 1620
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 Db 1561 tcttgttctcagcttcaacttcaagctgttacttgaatgaacacacttcaataatgaagtcg 1620
 QY 1621 AAATTTGATATATATGTAATGTAATGACTCAGTTTCTTGTGAGATCAATTTTCACAGTGTGC 1680
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 Db 1621 aaatttgatacatatgtgaaatcaatgactcagcttcttctgcagatcaaaatctcaagtcgctc 1680
 QY 1681 TTTCTATATCTGTGAGGTACACTCTTTATAGAAAGTTTCAAAAGTCTACGCTTCCTTTTC 1740
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 Db 1681 ttctgtataactgtgaggttacaaccttataagaagttcaaaaaggtctacgctcttcccttcc 1740
 QY 1741 TTTTCTAACTCCAGTGAAGTAATTTGGGCTCTGCTCAAGTTTGAAGAGTCTTATTTTGCACTG 1800
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1741 ttctctaactcagtgtaagtaatgtggttctcgtctcaagttgaaagagttcttatttgcactgt 1800
 QY 1801 TAGCCTGCGCTGTGTGAATTTGAGCAATCTATTTAACTGGCTTCAAGCCTCCCACTT 1860

Db 1801 tagctcgcgctgtgtgaatttgaccatccatcttaactgagcttcaagccctcccaacttc 1860
 QY 1861 CTTCAGCCACCTCTCTTTTTCAGTTTGGCTGACTTTCACACACCCTAGAGATCTCATGATGCCA 1920
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1861 cttcagccacactctcttcttcagttggtcgtaccttccacacactgaatctcctgaatgcca 1920
 QY 1921 AGCAAAAG 1980
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1921 agcaaaag 1980
 QY 1981 TTTCTTTTATGAGACCACTTCCTATTTCTTATGATCAATGTTTCTTTATGACGATATTA 2040
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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 QY 2041 TTATGTAAGAAACATCACTGAATGCTTACGTCGCAAGTGAACATCTTCTTATGATGATG 2100
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 Db 2041 ttagtaagaagaacacatcactgaatctagctgtgcaagtgacatctctcttgatgctatacg 2100
 QY 2101 AAGAGTTAAACAGGTGAGAGAAATTCCTGATTCATGCAATGAATGCTCTCCCTTCCCTG 2160
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 Db 2101 aagagttaaacaggtgtgagaatctccttgatctcacatgaaatgcttcccttccctg 2160
 QY 2161 CCCCCAGAACTTTTATTCACATTCCTAGATTCATATTCCTTTAAATTTGATCTCAGGC 2220
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2161 cccccaagaaacttatactcacttactagatctctacatatacttcttaaatctcctcagc 2220
 QY 2221 CTCCCTCAACCCCGACGGGGCCGCGACGACACTGCAATTC 2259
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2221 ctccctcaaccccgagggcgccgacacatgaaatcc 2259
 RESULT 5
 T30003
 ID T30003 standard; DNA: 2259 BP.
 XX
 AC T30003:
 XX
 DT 31-OCT-1996 (first entry)
 XX
 DE Human lymphocyte cell surface glycoprotein (HULHR) coding sequence.
 XX
 KW Immunoglobulin; transmembrane receptor; adhesion; targetting;
 KW diagnosis; therapy; drug delivery; antiviral; neuromodulator;
 KW immunomodulator; cell adhesion; graft rejection; inflammation;
 KW metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 129..1247
 FT /*tag= a
 FT /product= Lymphocyte cell surface glycoprotein.
 FT 129..242
 FT /*tag= b
 FT mat_peptide 243..1244
 FT /*tag= c
 PN US5514582-A.
 XX
 PD 07-MAY-1996.
 XX
 PE 23-FEB-1989; 89US-0315015.
 XX
 PR 22-NOV-1989; 89US-0440625.
 PR 23-FEB-1989; 89US-0315015.
 PR 16-DEC-1991; 91US-0808122.
 PR 08-DEC-1992; 92US-0986931.
 PR 21-JAN-1994; 94US-0185670.
 XX
 PA (GENTH) GENENTECH INC.
 PI Capon DJ, Lasky LA.

Db 1621 aaattgatacatatgtaataatgactagttctctgcagataaattcacgctgctc 1680
QY 1681 TTCTGTATAGTGTGAGGTACACTCTTATAGAAGTTCAAAAAGTCTACGCTCTCTTTC 1740
Db 1681 ttctgtatactgctggaagtaaacctctataagaagttcaaaaagttcacgctctcttc 1740
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Db 1741 ttcttaactccagtggaagtaatggggtctcgaagttcgaagttgaagatcttaattgcaatg 1800
QY 1801 TAGGCTGGCGCTCTGTGAATTTGACACATCTTATTAAGTCTGAGGCTTCCGACCTT 1860
Db 1801 tagcttcgctgctgtaaatggaaccatcttaacttaagttcctcaaggctcccccacctt 1860
QY 1861 CTTCAGCACACTCTCTTTTCTAGTGGCTGACTTCACACCTAGCATCTCATGTAGTGCCA 1920
Db 1861 cttaagccactctctcttcttaagttgctgactccacaactcgaalctcaltgagtgcca 1920
QY 1921 AGCAAAAGGAGAGAAGAGAATAGCCTGCCGCTTTTGTAGTTGGGGCTTTTGCTGT 1980
Db 1921 agcaaaaggagagaagagaagaataagctgcgctgttcttaagttgagggtctctgctgt 1980
QY 1981 TTCTTTTATAGACCCATCTCTTCTTATAGTCAATGTTCTTTTATACGATATTA 2040
Db 1981 ttcttttatagagaccatctctatacttcttaagttcaagttctcttatacagataata 2040
QY 2041 TTACTAAGAAACATCATGTAATGCTAGTGAAGTGAATGCTCTTGTATGATATAGG 2100
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QY 2101 AAGATTAAAGACAGTGGAGAAATTCCTTGAATTCACAAATGAATGCTCTCTCTCCCTG 2160
Db 2101 aagattaaagaaacagtgagagaataatcctctgaltcacaatgaaatgctcctctccctg 2160
QY 2161 CCCCCAGAACTTTTATTCACCTTACCTTACATTTCTTAAATTTGATCTCAGGC 2220
Db 2161 cccccagaactttatactcacttaccatctagatctacatactcttaaatcttcaatcaga 2220
QY 2221 CTGCTCAACCCGACGGGGCGGCGACGACACTGGAATTC 2259
Db 2221 ctgctcaaccccgacggggcgcgacgacactggaatctc 2259

RESULT 6
VI9012
ID VI9012 standard. DNA; 2259 BP.
XX
AC VI9012;
XX
DT 17-AUG-1998 (first entry)
XX
DE Homo sapiens lymphocyte homing receptor (LHR) gene.
XX
KW lymphocyte homing receptor; LHR; HuLHR; organ; graft; rejection;
KW treatment; inflammatory disorders; rheumatoid arthritis;
KW autoimmune diseases; lymphoma metastasis; control; lymphocyte;
KW accumulation; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 129..1247
FT FT /*tag= a
FT FT /product= lymphocyte homing receptor
XX
XX US5714147-A.
PN
XX
XX 03-FEB-1998.
PD
XX
XX 23-FEB-1989; 89US-0315015.
PF
XX
XX 22-NOV-1989; 89US-0440625.
PR
XX 23-FEB-1989; 89US-0315015.

PR 19-DEC-1991; 91US-0808122.
PR 08-DEC-1992; 92US-0986931.
PR 21-JAN-1994; 94US-0185670.
PR 26-MAY-1995; 95US-0451848.
XX
PA (GERTH) GENENTECH INC.
XX
XX
PI Capon DJ, Lasky LA;
XX
DR WPI: 1998-129805/12.
DR P-PSDB: W37781.
XX
PT Prevention of lymphocyte attachment to endothelial cells - using
PT chimeric molecule comprising lymphocyte homing receptor and
PT immunoglobulin constant region
XX
PS Disclosure: Fig 1; 43pp: English.
XX
CC The sequence is that encoding a human lymphocyte homing receptor
CC (LHR) which may be used in the construction of a chimeric molecule
CC comprising an LHR fused at its C terminus to the N terminus of an
CC immunoglobulin constant region. This can be used for the prevention
CC of lymphocyte attachment to endothelial cells. Such a method may
CC be used for preventing organ or graft rejection, for treating
CC inflammatory disorders, e.g. rheumatoid arthritis or other
CC autoimmune diseases, for controlling lymphoma metastasis and
CC for treating conditions in which there is an accumulation of
CC lymphocytes.
XX
SQ Sequence 2259 BP; 635 A; 516 C; 489 G; 619 T; 0 other;
Query Match 99.9%; Score 2255.8; DB 19; Length 2259;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2257; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAATTCAGTGTGCTGGCTTCCTCAGCTGACGACAGACACTCCCTTTGGCAAGACCT 60
Db 1 gaattccagtgtgctgtgctctcctcactcgcagacacactcctcttggaagacct 60
QY 61 GAGACCCCTTGCTGTAAGTCAAGAGGCTCAATGGGCTCGAAGAATAGAGAGACCA 120
Db 61 gagacccttgctgctaagtcgaagagctcaatggtctgagaagactagagaagaccaa 120
QY 121 GCAAAAGCATATATTTTCATGAGAAATGTAGACACCCAGAGGACTTATGAACTCT 180
Db 121 gcaaaagcatatatttccatcgaaatgtcagagacaccacagagacttatagaaactct 180
QY 181 TCAAGTTGTGGGGTGAGCAATGCTCTGTTGTAATTCCTGGCAATCATGGAACCTACT 240
Db 181 tcaagttgagggggtgagcaatgctctgttgtaatttcctggcaatcatggaacctact 240
QY 241 GCTGGACTTACCATTAATTTCTGAAAACCCATGAATGAGGCTAGAAATTTCTGCC 300
Db 241 gctggacttaccattatctcgaaaaaccatgaaactcgtgaaaggtcagaagactctgccc 300
QY 301 GAGACATTTACAGATTTTACTTGGCATACAAACAGGCGGAATTGATATCTGGAGA 360
Db 301 gagaacaattacagattttacttggcatacaaacaggcggaattgagatctggaga 360
QY 361 AGACTTCGCGCTTCAAGTGTCTTACTACTGATAGCAATCGGAAGATAGAGGAATAT 420
Db 361 agacttcgctctcaagtgcttctactactcgtgataaggaatccggaagatagagaatat 420
QY 421 GGAGCTGGGTGGGAACCAAAATCTCTCACTGAAGAAGACGAGAACTGGGAGATGGTG 480
Db 421 ggaactgggtgggaaccaaattctctactactcgtgataaggaatccggaagatagagaatat 480
QY 481 AGCCCAACACAAAGAAGAACAGAGAGACTCGTGGAGATTTATATCAAGAAACAAG 540
Db 481 agcccaacacaagaagaacaagaagactcgtggagatcttatacaagaagaacaag 540
QY 541 ATGCAGCAATGGAAGCATGACCCCTGCCAACAATCAAAGCAGCCCTCTGTAAACAG 600

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Db 541 atgcagagcaaatggaagatgacgctgcacaaactaaagcagccctcgttacacag 600
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Db 601 ctcttgcagccctcgttacatgcaagcagcccaatggaatgtagaaatcaatacaatac 660
QY 661 ACACCTGCAACTGTGATGTGGGTACTAATGGCCCAAGTGCAGTGTGATTCAGTGTG 720
Db 661 acacatgcaacttgaatgtagggtactatgcgcccagtgtaagcttctgattcagtg 720
QY 721 AGCCTTGGAGGCCCAAGAGCTGGGTACATGACATGACTGTAACCCCTTTGGAACCTGA 780
Db 721 agccttggagggcccagagcctgggtacacatgacttcaaccccttggaaacttca 780
QY 781 GCTTACGCTACAGTGTGCTTACGCTGCTGAGAGAACAACTTAACCTGGGATTTGAAG 840
Db 781 gcttcagctcacagtgctcctcagctgctcgaaggaaacttaactgagatcgag 840
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Db 841 aaacacacctgtagacattggaactggtcaatctccagaaacacacctgtaagtgat 900
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QY 961 GCTTACGCTTACCTCTGATGATGATCTGCTGCTGAGAGAACGTAGTTAATTTGGA 1020
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Db 1021 agaagaanaaaccaatctgtaatcattgtaactggtcaaatctcagtaataatg 1080
QY 1081 AATTGAGACAAAAGTTTCTCAATGATTAAAGAGGGGATTAATACCCCTCTTCATTCAG 1140
Db 1081 aattgacaaaaagttctccaatgattaaaggaggtgattataaacccctctcctcag 1140
QY 1141 TGGCAGTATGTTACTGTCATCTCTGCGTTGGCATTTATCATTTGGCTGGCAAGGAT 1200
Db 1141 tggcagtaatgattactgcatctcctcgtgttgcatattatcatttgcgtgcaagg 1200
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Db 1201 taaaaaaggagcaagaataccaagaggaatgaaatgaacccatataatcgccctt 1260
QY 1261 AAGAGAAAATTTCTGAATACTTAAATAATCAGAGATCCTTTAATCTTCATGAAGGT 1320
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Db 1321 ttgtgtgtggcacctctacagtcataaacatgaaagtgtgtccctcagtgatctgg 1380
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Db 1381 atttctacccgaccaaagatctcctcagcttccatttcgcccctcatcttccctaac 1440
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Db 1441 ccagcccaagtggttatacagctcagcttcttcttcttgaggagaaacaataa 1500
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Db 1501 gaccataaggaaagatcattgtaataaagatggtgacttgcctctctctgac 1560
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Db 1621 aaattgtacataatgtaataatgtaactcagtttcttgcagatcaaatcactcagtc 1680
QY 1681 TTCTGTATACGTGTGAGGTACACTTTATAGAAAGTTCAAAAAGTTCTACGCTCTCTT 1740
Db 1681 ttctgtatactgtggaagttacactcttataagaagtccaagaatctcagctctcttc 1740
QY 1741 TTTTCACTCCAGTGAAGTAAATGGGGTCCGCTCAAGTTGAAAGAGTCTATTGTGACTG 1800
Db 1741 ttcttaactccagtgaaatlaagggtccctgctcaagttgaaagagtcctatttgac 1800
QY 1801 TAGCCTCCGCTGTGTGAATTTGACATTCCTATTATACCTGCTTACGGCTCCGCCACT 1860
Db 1801 tagcctcgctgtgtgaatgtggacactctatttaactgtctcaggtccctccacct 1860
QY 1861 CTTACGCACTCTCTTTTTCAGTGGCTGACTTCACACCTAGACATCTCATAGAGTCCA 1920
Db 1861 cttaagcacctctcttcttcagttgctgtaacttccacactagcatctcaatgag 1920
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Db 1921 agcaaaaggagagagagaaataagcctgcgcggttctttagttgggggttctgt 1980
QY 1981 TTCTTTTATGAGACCCCATCTCTATTCTTATAGTCAATGTTCTTTATCAAGATATA 2040
Db 1981 ttctctttagagagcccatctctatttcttatagtaaatgttctcttatacagata 2040
QY 2041 TTAGTAGAAAACATCATCTAAATGCTAGTGCATGACATCTCTTGTATGTCAATATG 2100
Db 2041 ttagtgaagaaacatcaatgaaatgctagctgcaagtgcacatctctttagtcatag 2100
QY 2101 AAGAGTTAAACAGGTGAGAGAAATTCCTTGATTTCAACAATGAATAAGCTCTTCCTCC 2160
Db 2101 aagagttaaacacaggtgaggaataatctcttgatccaaatgaaatgtctccctcc 2160
QY 2161 CCCCAGACACTTTTATTCACCTTACTAGATTTCTACATTTCTTAAATTCATCTCAG 2220
Db 2161 cccccagaaacttataccacttaccatgattctacatcttcaattcaattcaatcc 2220
QY 2221 CTCCTCAACCCGAGGGGCGCCAGCACATGAGATTC 2259
Db 2221 ctccctcaacccagggcgccagcacacatcgaaatc 2259
RESULT 7
Q43154
ID Q43154 standard; cDNM: 2259 BP.
XX
AC Q43154;
XX
DT 08-OCT-1993 (first entry)
XX
DE Human Lymphocyte Homing Receptor coding sequence.
XX
KW HuLHR; lymphocyte binding inhibition; lymphoma metastasis;
KW transplant rejection; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 129..1247
FT FT /*tag= a
FT FT /product= HuLHR
FT FT 186..224
FT FT /*tag= b
PM US5216131-A.
XX
PD 01-JUN-1993.
XX
PF 23-FEB-1989; 89US-0315015.
XX
PR 23-FEB-1989; 89US-0315015.
PR 31-OCT-1991; 91US-0786149.
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XX (GETH) GENENTECH INC.
XX
XX Lasky LA, Rosen SD, Singer MS, Stachel SE, Yednock TA;
XX WPI: 1993-188588/23.
XX P-PSDB: R37960.
XX
XX Human and murine lymphocyte homing receptors to treat graft
XX rejection and inflammation - comprise carbohydrate binding,
XX epidermal growth factor and complement binding domains
XX
XX Example 2; Fig 1; 32pp; English.
XX
XX A human peripheral blood lymphocyte cDNA library in lambda gt10 was
XX screened with a 2.2kb EcoRI insert of the murine Me11a antigen clone
XX (i.e. a murine LHR sequence). The largest EcoRI insert (2.2kb) was
XX isolated and sequenced. The ORF codes for 372 amino acids with a mol.
XX wt. of approximately 42,200. Comparison of the huLHR cDNA with the
XX previously determined murine LHR sequence (Q43155) showed 83%
XX homology.
XX
XX
XX Sequence 2259 BP; 635 A; 515 C; 490 G; 619 T; 0 other:
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 2256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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DB 1 gaattccagtgctgcttcctccaccctgcagcacagcacactccttggcaagagacct 60
OY 61 GAGACCCCTTGTGCTAAGCAAGAGGCTTAATGGCTGCAGAAAGCAATGAGAGGACCAA 120
DB 61 gagacccttgtgctaaagccaagagctcaatgagctgagaaagaaactagaagaagaccaa 120
OY 121 GCACACCATATATATTTTCATGAGAAATGTCAGAGCACCACGAGGAGCTTATGGAATCTT 180
DB 121 gcaaacgcatatatttccatcggaatgtcagagcaccagagagactctatggaacatctc 180
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DB 181 tcaagttgtgggggtgacaaatgctctgtgtgatttctggcagcatggaacctact 240
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DB 241 gctggacttaccatttatttctaaaaacccatgaaactggcaaaaggcttagaagattctcc 300
OY 301 GAGACAAATTACACAGATTATGTCATACAAACAAAGCGGAATTGATATCTGAGAGA 360
DB 301 gagacaattacacagatttattgtcattacaaacaaagcggaattgatatcttgagaga 360
OY 361 AGACTGTGCTTCAAGTCGTTCTTACTACTGATAGAAATCCGGAAGATAGAGAGAAATAT 420
DB 361 agactgtgcttcaagtcgttcttactactgatalagaaatccggaaagttagagaaatatt 420
OY 421 GGAGGTGGGTGGCAACCAAAATCTCTCACTGAAGAAGCAGACAACTGGGGAGATGGTG 480
DB 421 ggaggtgggtggcaaccaaattctctcactgaagaagcagaaactggggagatggtg 480
OY 481 AGCCCAACAAACAGAAAGAGAGAGCTGCTGAGATCTATATCAAGAAACAAAG 540
DB 481 agcccaacaaacagaaagagagagagactcgtgagagattatatacaagaaacaaag 540
OY 541 ATGACAGGCAAAATGAGAGATGAGCCTGCGCAAAACTAAAGCAGCCCTCTGTTACACAG 600
DB 541 atgacaggcaaaatgagagatgagcctgcgcaaaactaaagcagccctctgttacaacag 600
OY 601 CTTCCTGGCAGCCCTGGTGCATGACAGTGGCCATGGAGAAATGTTAGAAATCATTAATTC 660
DB 601 ctctctggcagccctgggtgcattgacagtgggcattggagaaatgttagaaatcataatc 660

OY 661 ACACCTGCNAAGTGTGATGTGGGTACTATAGGCCCCAGTGCAGCTGTGATTCAGTGTG 720
DB 661 aaacctgcnaagtgtgatgtgggtactatagggccccagtgcagctgtgatctcagtg 720
OY 721 AGCCTTTGAGGCCCCAGAGCTGGGTACCAGAGCTGATCTACCCCTTTGGAACCTTCA 780
DB 721 agcctttgaggccccagagctgggtaccagagctgatctacccctttggaaccttca 780
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DB 841 aaacctgtgagaccatttggaaactgatgctccagaaacaaacctgcaaggtatc 900
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DB 901 agtgtgagcctctatagcaccagatTTTGGGATCATGAACTGTAGCCATCCCTggcca 960
OY 961 GCTTCAGCTTAACTCTGATGCTACCTTCATCTGCTCAGAGAGAACCTGATTAATTGGGA 1020
DB 961 gcttcagcttAACTCTGATGCTACCTTCATCTGCTCAGAGAGAACCTgattaaattggga 1020
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DB 1021 agaagaaaccatTTGTGAATCATCTGGAATCTGGTcaaaatctgtcatatATGTCana 1080
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DB 1081 aattggacaaaagTTTCTCAATGATTTAAGAGAGGTGATTAATACCCCTcttcatttccag 1140
OY 1141 TTGGCATGATGTTACTCTGATTTCTGGGTGGCATTTATCATTTTGGCTGGCAGAGCAAT 1200
DB 1141 tggcatgatgTTACTCTGATTTCTGGGTGGCATTTATCATTTTGGCTggcagagcaat 1200
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DB 1201 taAAAAAGGCAAGAAATccAAAGAGAGTATGAATGAGCCCATATTAATTCGGCCCTggtg 1260
OY 1261 AAAGAAAATTTCTTGAATATCAAAAATCATGAGATCTTTAAATCCTTTCATGAAACGTT 1320
DB 1261 aaagaaaatTTCTTGAATATCAAAAATcatGAGATCTTTAAATCCTTTCATgaaacgTT 1320
OY 1321 TTGTGTGGTGGCAGCTCTTACAGTCAAAACATGAAGTGTCTCTTCAGTACATCTGGGAG 1380
DB 1321 ttgtgtggTGGCAGCTCTTACAGTCAAAACATGAAGTGTCTCTTCAGTACATctgggag 1380
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DB 1441 cccagcccaAGGTgttATACAGCTCAGCTTTTGTCTTTCTGAGAGAGAAACAAATta 1500
OY 1501 GACCAATAGGGAAGAGATTCATGTCGATTAATGAAGATGCGCTGACCTTCTTTCTTAC 1560
DB 1501 gaccaatAGGGAAGAGATTCATGTCGATTAATGAAGATGCGCTGACCTTCTTTctTAC 1560
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DB 1561 tcttGTTCAGTTTCAATTAAGTGTGCTGATGTCAGACACACTTAAATGAAAGTgc 1620
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DB 1621 aaatTTGATATATGGAATATGGAATGCACTtctTTTTCAGATCAAAATTTTCacgctgTC 1680
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Db 1741 ttcttaactccagtcgaaagtaagtggtccctcccaagttgaagagctccatttcgacgtg 1800
QY 1801 TAGCCTCGCCGCTGTAATTTGGACCATCCATTTAACTGGCTTCAGGCCGCCACCTTT 1860
Db 1801 tagctcgcgcgtctgtaatttgacacatccatttaactcgtctcagcctcccaacctt 1860
QY 1861 CTTCAGCCACCTCTCTTTTTCAGTTGGCTGACTTCCACACCTAGCATCTCATAGTAGTCCA 1920
Db 1861 cttaagcaccctctctcttcagttgctgactccacacacctaagcatctcatagtgcca 1920
QY 1921 AGCAAAAGAGAGAGAGAAATAGCCGCGCGGTTTTTTAGTTGGGGGTTTTGCTGT 1980
Db 1921 agcaaaaagagagaaagaaatagccgcgcggtttttagtttggtggtgttgcgtgt 1980
QY 1981 TTCCTTTTATGAGACCCATTTCCATTTCTTATATGATCAATGTTCTTTTATACGATATTA 2040
Db 1981 ttccctttatgagaccatctccattctctattctatagtaaatgcttctcttccacgatatta 2040
QY 2041 TTAGTTAAGAAAACATCATCTGAATGCTAGCTGCAGTGCATCTCTTGATGTCAATAGG 2100
Db 2041 tttagtaagaanaacatcacgtaaatgttagctgcaagtgcacatctctttagtgcataatg 2100
QY 2101 AAGAGTTAAACAGAGTGAGAAATTCCTGATTCACAAATGAATGCTCTCCCTTTCCCTG 2160
Db 2101 aagagttaaacaagctggaagaaatctcctgattcacaagaatgctccttccctctg 2160
QY 2161 CCCCCAGAACTTTTATCCATTACCTAGATTCTACATATTTTAAATTTTCATCTCAGGC 2220
Db 2161 cccccagaaactttatccacttaactagatctacatatctcttaatttcaatctccagtc 2220
QY 2221 CTCCTTCACACCCGACGGGCGCCGACGACACTGGAATTC 2259
Db 2221 ctccctcaacccacgcgcgcgcagcacactgtaattc 2259

RESULT 8
Q12118
ID Q12118 standard; DNA: 2259 BP.

AC Q12118;

DT 09-SEP-1991 (first entry)

DE Sequence encoding human lymphocyte cell surface glycoprotein (LHR).

KW Ligand binding partner; lbp; stable plasma protein; spp; antiviral;

KW immunomodulatory; neuromodulatory; receptor mediated abnormality; ds.

OS Homo sapiens.

XX Location/Qualifiers

FT CDS

FT sig_peptide

FT mat_peptide

FT

XX W09108298-A.

XX 13-JUN-1991.

XX 21-NOV-1990; 90WO-US06849.

XX 22-NOV-1989; 89US-0444625.

XX (GETH) GENENTECH INC.

XX Capon DJ, Lasky LA;

XX WPI; 1991-193202/26.

XX P-PDB; R12469.

XX New hybrid immunoglobulin(s) - for use as diagnostic reagents for
PT ligand binding molecules and to treat organ and graft rejection
PT and inflammation.
XX
PS Disclosure: Fig 1; 67pp; English.
XX
CC The gene product may be used as a ligand binding partner in combina-
CC tion with a stable plasma protein eg. IgG1-IgG4, IgA, IgE, IgD or IgM.
CC The fusion product is joined by N- or C-terminal groups, preferably
CC the N-terminal of the FC region of the spp is linked to the C-terminal
CC of lbp. They may be used to provide antiviral, immunomodulatory
CC and neuromodulatory treatment as well as in treatment of receptor
CC mediated abnormalities.
XX
SQ Sequence 2259 BP; 634 A; 516 C; 487 G; 618 T; 4 other;

Query Match 99.7%; Score 2251.8; DB 12; Length 2259;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2253; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GAATTCCAGTGTGCTGGCTTCTCCTCAGTCAGCAGCAGCAGCTCTTGGCAAGGACCT 60
Db 1 gaattccagtgctggcttctcctcagtcagcagcagcagcagcagcagcagcagcagcagc 60
QY 61 GAGACCTTGTGTTAGTCAAGAGGCTTCATTTGGCTGCGAGAAACTAGAGAGACCAA 120
Db 61 gagaccttgtgttagtcaagagggcttcatttggctgcgagaaactagagagaccaa 120
QY 121 GCAAAAGCATGATATTTTCATGGAATGTGAGAGCAGCAGCCGAGAGGACTTATGGAACATCT 180
Db 121 gcaaaagcatgatattttcatggaaatgtgagagcagcagccgagagacttatggaacatct 180
QY 181 TCAAGTTGTGGGGTGAGCAATGCTGTGTGATTTCTGGACATCATGCAACTACT 240
Db 181 tcaagttgtggggtgagcaatgctgtgtgatttctggacatcatgcaactact 240
QY 241 GCTGACTTACCATTTATTCGAAAACCCATGAACTGAGAGGCAAGGCTTAAACATTTCTGCC 300
Db 241 gctgacttacatttatctcgaanaacccaatgaaactgagaaaggcttaagaattctgcc 300
QY 301 GAGACAATTACAGAGATTTAGTTGCCATACAAACAAGCGGGAATTTGATTTGAGAGA 360
Db 301 gagacaatttacagagatttagttgccatatacaaaagcggaattgatatctggaga 360
QY 361 AGACTCTGCCCTTCAGTGTCTTACTAGTGGATAGGAATCCGGAAGATVAGAGAGATAT 420
Db 361 agactctgcccttcagtgttctactactgtagaagaaatccggaagatagaagaatat 420
QY 421 GGAGCTGGGTGGGAACAATAATCTCTACGTGAAGACGAGAACTGGGAGATGGTG 480
Db 421 ggagctgggtgggaacaataatctctacgtgaagacgagaaactgggagatgggtg 480
QY 481 AGCCCAACAACAAGAAACAAGAGAGACTGCGTGAATCTATATCAAGAGAAACAAG 540
Db 481 agcccaacaacaagaagaacaagagactgcgtagaattctatatacaagagaacaag 540
QY 541 ATGCAGCAAAATGAGAGATGACGATGCGCTGCGACAACATAAGCAGCCCTGTTATACAG 600
Db 541 atgcagcaaaatgagagatgacgatgcgctgcgacaacataagcagccctgttatacag 600
QY 601 CTTCCTGGCAGCCCTGCTATGATGAGTGGCATGGAATGTTAGAAATCATCAATATC 660
Db 601 ctctctggcagccctgctatgatgagtggtggaattgttagaaatcatcaatattc 660
QY 661 ACACCTGCAACTGTATGTGSGGTACTATGGGCCCCAGCTGATGTTGATTAAGTGTG 720
Db 661 acacctgcaactgtatgtsgggtactatgggcccccagctgatgttgaattagtggtg 720
QY 721 AGCCTTTGAGAGGCCAGAGAGCTGGGTACCATGAGACTGTACTACCCCTTTGGAAGCTTCA 780
Db 721 agcctttgagagggccagagagctgggtaccatgagactgtactacccctttggaacttca 780

[illegible]

QY	1861	CTTCAGCCACCTCTCTTTTTCACGTTGGCTCACTTCCACACCTTACGATTCGATCTGCCA	1920
QY	1861	CTTCAGCCACCTCTCTTTTTCACGTTGGCTCACTTCCACACCTTACGATTCGATCTGCCA	1920
Db	1861	cttcagccacctctctcttcttcagcttgctgacttccaccactagcaltgcatgagtgcca	1920
QY	1921	AGCAAAAGACAGAAAGAGAAATAGCTGCGGGTTTTTACTTTGGGGGTTTTGCTGT	1980
Db	1921	agcaaaagagagagagagaaatagccgcgcggtcttctgacttgagggtcttgctgct	1980
QY	1981	TTTCCTTTTATAGAGCCCATTCCTCTATTTCTTATAGTCATAGTTTCTTTATCAGATATTA	2040
Db	1981	ttctcttctatgagaccatcttcctacttctcttaagtcataagcttctcttatacgaatata	2040
QY	2041	TTTAGTAGCAAAATCTCACTGAATATGCTAGTCGACAGTACATCTCTTATGTCATATTC	2100
Db	2041	tttagtaagaataacatcacatcgaaatgctagctgaagtgacatctctcttgatgcatatag	2100
QY	2101	AAGATTAAACAGGTGGAGAAATTCCTTATTCACAAATGCTCTCTTCCCTCG	2160
Db	2101	aagagcttaaaacagtgagagaaatctctgattcacaagtgaaatgctctctctccctcg	2160
QY	2161	CCCCCAGACCTTTTATTCACCTTACCTAGATTACATATTTCTTAAATTTCAATCTCAGGC	2220
Db	2161	coccacagacttctatctcaacttcaactctagatctcaacatctcttataatcttcaatccaggc	2220
QY	2221	CTTCCCTCAACCCACAGGGGCGCCGACGACACTGTGAATTC	2259
Db	2221	cttcctcaacccacaggggcgcgcagcacactgaaatcc	2259
RESULT	9		
ID	Q23623	standard; DNA; 2260 BP.	
XX	Q23623:		
AC	Q23623:		
XX	01-SEP-1992	(first entry)	
DT			
XX		Human lymphocyte homing receptor gene.	
DE			
XX			
KW		HuLHR: LHR: binding: endothelium: immunogens: graft: organ: ss:	
KW		Rejection: Inflammation; Rheumatoid arthritis; Lymphoma metastasis.	
XX			
OS		Homo sapiens.	
XX			
FN		Key	Location/Qualifiers
FT		CDS	129..1248
FT			/*tag= a
XX			
PN		US5098833-A.	
XX			
PD		24-MAR-1992.	
XX			
PE		23-FEB-1989; 89US-0315015.	
XX			
PR		23-FEB-1989; 89US-0315015.	
XX			
PA		(REGC) UNIV OF CALIFORNIA.	
XX			
PI		Lasky LA, Rosen SD, Stachel SE, Singer MS, Yednock TA:	
XX			
DR		WPI; 1992-123385/15.	
DR		P-PSDB; R22802.	
XX			
PT		New DNA encoding at least one domain of lymphocyte homing	
PT		receptor - useful for treating graft rejection, inflammation,	
XX		etc.	
PS		Claim 3; Fig 1; 32pp; English.	
XX			
CC		The DNA sequence was obt'd. by screening an oligo dt primed lambda	
CC		gt10 cDNA library derived from human peripheral blood lymphocyte	
CC		mRNA obt'd. from primary cells, with a 2.2 kb EcoRI insert of the	
CC		murine Mel 14 antigen cDNA clone. 12 positive plaques were isolated	

50 Sequence 2260 BP; 636 A; 518 C; 487 G; 619 T; 0 other;

Matches 2244; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 661 acacctgcaactgtgatgtgggtactatggtggcccaagtgtcagcttgatcattcagtttg 720

QY 1801 TAGCCTCGCGTCTGTGAATTGGACCATCCTATTAACTGGCTTCAGGCTCCCACTT 1860

|||||
Db 1801 tagctcgcgcgtcgtgaattgaccatccatttaactgcttcaaggcctccaccct 1860
OY 1861 CTTGAGCCACGCTCTTTTTCAGTTGSGCTGACTGCTCCACACCTAGACATGTCATGAGTGCAC 1920
Db 1861 cttaagcaacctctcttcttaagtgctgacctccacacgctatgcatgagtgcca 1920
OY 1921 AGCAAAAGAGAGAGAGAGAAATFAGCCCTGGCGGGTATTTAGTTTGGGGTATTTGCTGT 1980
Db 1921 agcaaaaggagagagagagaaatagcctgcgsgcttcttaagtltggggtcttgccgct 1980
OY 1981 TTTCTTTTATAGAGACCCATTCCTATTTTCTTATATGCAATGTTTCTTTATATGCAATATTA 2040
Db 1981 ttctcttatgagaccctctcttcttctatagcaaatgttcttcttatacagcatla 2040
OY 2041 TTAGTAAGAAACATCATGAAATGCTAGTGCAGTGCAGTGCATGCTGATGCTATAGG 2100
Db 2041 tttagtaagaataaacacacacgaaatgctagtcgcaagtgcacatctctcttgatgcatag 2100
OY 2101 AAGAGTTTAAACAGGTGAGAGAAATTCCTTGAATTCACAAATGAAATGCTTCCTTCCCTG 2160
Db 2101 aagagtttaaaacaggctgagaaatctccttgatctacaatgaaatgctctctctccctg 2160
OY 2161 CCCCCAGACGCTTTTATATCAGCTTACCTAGATTCATATTCCTTTAAATTCATCTCAGGC 2220
Db 2161 cccccagaccttatactcaactacatagatctacatatcttcttaaatctcaatcagc 2220
OY 2221 CTCCCTCAACCCGACGGGGCGCCAGCA 2248
Db 2221 ctccctcaaccacagggccgca 2248

RESULT 10
O24987
ID Q24987 standard; DNA: 2262 BP.
XX Q24987;
XX
DT 22-NOV-1992 (first entry)
XX
DE Sequence encoding human lymphocyte cell surface glycoprotein
DE (HULHR).
XX
KM Lymphocyte cell surface glycoprotein; ligand binding protein; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 129..185
FT /*tag= a
FT sig_peptide 186..242
FT /*tag= b
FT mat_peptide 143..1247
FT /*tag= c
XX
XX US5116964-A.
XX
XX 26-MAY-1992.
XX
XX 22-NOV-1989; 89US-0440625.
XX
XX 23-FEB-1989; 89US-0315015.
XX PR 22-NOV-1989; 89US-0440625.
XX
XX (GETH) GENENTECH INC.
XX
XX Capon DJ, Lasky LA;
XX
XX WPI: 1992-199589/24.
XX DR P-PSDB; R24026.
XX
XX Nucleic acid encoding polypeptide fusions - comprising ligand
XX binding partner protein and immunoglobulin chain, for use in
PT

PT diagnosis and therapy
XX
PS Disclosure: Fig 1-1 - 1-3; 43pp; English.
XX
XX LHR mediates the binding of lymphocytes to the endothelium of
CC lymphoid tissue. Full length cDNA clones and DNA encoding the human
CC and the murine LHR (HULHR and MLHR, respectively) have been
CC identified and isolated (see Q24987 and Q24988). LHR is a
CC glycoprotein which contains the following protein domains: a signal
CC sequence, a carbohydrate binding domain, and epidermal growth
CC factor-like (egl) domain, at least one and preferably two complement
CC binding domain repeat, a transmembrane binding domain (TMD), and a
CC charged intracellular or cytoplasmic domain. LHR is used as the
CC ligand-binding partner in fusion polypeptides with an immunoglobulin,
CC for use in diagnosis and therapy.
XX
SO Sequence 2262 BP: 635 A: 518 C: 488 G: 621 T: 0 other:

Query Match 99.2%; Score 2241.2; DB 13; Length 2262;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2256; Conservative 0; Mismatches 3; Indels 3; Gaps 1:

OY 1 GAATTCAGGTGTGCTGCTTCCTTCACCTGCAGACAGACACACTCCCTTTGGCAAGACT 60
Db 1 gaattcaggtgtgctgcttcccttcacccgcagcacagcaactccttggcgaagact 60
OY 61 GAGACCCCTTGCTGCTAAGTCMAAGAGGCTCATATGGCTGCAGAAATGAGAGACCA 120
Db 61 gagaccttgctgctagctcaagagctcatatggtctgcaagaactagagagaccaa 120
OY 61 GCAAGCCATGATATTTCCATGGAATGTCAGAGACCCAGCGGATATGGAACATCT 180
Db 121 gcaagccatgatatcttcacatggaatgctcagagacccagaggaactataggaacatc 180
OY 181 TCAAGTTGTGGGGTGGACAATGCTCTGTGTGATTTCTGTGCACATGTAACCTACT 240
Db 181 tcaagttgtggggtggacaatgctctgtgtgatttctgtgtcgcacatcgtgaacctact 240
OY 241 GCTGACTTACCATTTATCTGAAAACCATGTAAGTGGCAAAAGGCTGTGAAGATTCTCC 300
Db 241 gctgacttacatcttcttgaaaaccatgtaagtggcaaaaggctgtgaagattctgcc 300
OY 301 GAGACAATTACACAGATTTAGTTGGCATTAACAAAGCGGAATTTAGTATCTGAGCA 360
Db 301 gacacaattacacagatTTAGTTGGCATTAACAAAGCGGAATTTAGTATCTGAGCA 360
OY 361 AGACTTGCCTTCAGTGTCTTACTACTAGATAGAAATCCGGAAGATAGAGAGAAATAT 420
Db 361 agacttgccttcagtgcttctactactatgataagaaatccggagatagagaaatct 420
OY 421 GGAGCTGGGTGGGAACCAAAATCTCTCACTGAAGAAAGCAAGACTGGGAGATGTTG 480
Db 421 ggagctgggtgggaaccaaATCTCTCACTGAAGAAAGCAAGACTGGGAGATGTTG 480
OY 481 AGCCCAACACAGAGAAAGAAAGAGGACTGCTGGAGATCTATATCAAGAAACAAAG 540
Db 481 agcccaacacagagaaAGAAAGAGGACTGCTGGAGATCTATATCAAGAAACAAAG 540
OY 541 ATGCAAGCAAAATGGAACGATGACGCTGCCAACAACTAAAGGACCCCTCTGTTACACAG 600
Db 541 atgcaagcaaaATGGAACGATGACGCTGCCAACAACTAAAGGACCCCTctgttacaag 600
OY 601 CTCTTGCCAGCCCTGCTCATGCACTGCGCATTGAGAAATGTTGAAATTCATTAATC 660
Db 601 ctcttgccagccctgctcatgcatgctgagtcagtcgaagaaatctcaataatc 660
OY 661 ACACCTGCAACTGTGATGTGGGTACTATGGCCCACTGACGTTGCTGATTAGTGTG 720
Db 661 acacctgcaactgtgattgtgggtactatggcccaactgacgTTGCTGATTAGTGTG 720
OY 721 AGCCTTGGAGCCCAAGAGCTGGTACCATGAGACTGTACTACCCCTTTGGAACATTC 780
Db 721 agccttggagcccaAGAGCTGGTACCATGAGACTGTACTACCCCTTTGGAACATTC 780

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Db 721 agccttggagggcccaagagctgggtaacatggaactgtaactaccaccttggaaacttca 780
Qy 781 GCTTCAGCTCAGAGTGTGCTCTTCAGCTGCTCTGAAAGAAACAATCTTAACGGGATTGAAG 840
Db 781 gcttcagctcaagtgatgagcttccagctgagctcgaaggaacaacttaacatgaggttgaag 840
Qy 841 AAACCCACTGTGAGACCATTTGGAAACGTGTCATCTCCAGAACCAACCTGTCAAGTGAATTC 900
Db 841 aaaccacctgtgagacatlttgaaactgtaactcctcagaaaccaactgtcagaatgatac 900
Qy 901 AGTGTGAGCCCTCTATGACGACCCAGATTTGGGGATCATGAAGACTGTAGCAATCCCTGGCCA 960
Db 901 agtgtgagccctctacacagaccagatlttgggatacgaactgtgaacatccctcggcca 960
Qy 961 GCTTCAGCTTACCTCTGATGATGATCTTCATCTGCTCAGAAAGACAGTGAATTAATGGGA 1020
Db 961 gcttcagcttacctcctgcatgtaacctcactcgtccagaagaactgagttcaattgggga 1020
Qy 1021 AGAAGAAACCATTTTGGAAATCATCTGGAATCTGTGCAAAATCTCAATTCGAATTCGCAAA 1080
Db 1021 agaagaaacacatlttgaaatcatctggaatctgtaacatccctagccaataatgtcaca 1080
Qy 1081 AATTGCAAAAGTTTCTCATGATTAAGAGGGTGAATTAATACCCCTCTTCATCTCCAG 1140
Db 1081 aattgcaaaaagtcttctcaatgataaagagagtgatataaacccctctcatccag 1140
Qy 1141 TGGCAGTCATGTTACTGCAATTCCTGTGGGTGGCATTTATCATTTTGGCTGGAGAGAT 1200
Db 1141 tggcagtcatagttactgatactctcgtggttgcatltaactlttggctggaagagat 1200
Qy 1201 TAAAAAAGGCAAGAAATCCAGAGAGATGATGAATGCCATATTAAATCGCCCTTGGTG 1260
Db 1201 taaaaaaggcaagaaatccaaagaaagatgaalgaalgaacacataataacgcctctggg 1260
Qy 1261 AAGAAAA---TTCCTGGAATCTAAAAATCATGAGATCTTAAATCCTTCATGAAG 1317
Db 1261 aagaanaatctctcttgagataactaaatacatgagatcctttaaactccttcaagaac 1320
Qy 1318 GTTTGTGTGGTGGACCTCCCTCACTGCAACATGAAGTGTGCTTCAGTGCATCTGGG 1377
Db 1321 gtttgtgtggtggacccctcctcaatgataaacaatgaatgtgtccttcaatgacatctgg 1380
Qy 1378 AAGATTTTACCCGACCAACAGTTCCTTCAGCTTCATTTGGCCCTCATTTATGCCCA 1437
Db 1381 aagatttcaaccgacaaagcttctcctcagcttccatcttgcgccctcatltaaccctca 1440
Qy 1438 ACCCCAGCCCAAGAGTGTATACAGCTCAAGCTTTTGTCTTTCTGAGAGAAACAA 1497
Db 1441 accccagcccaagagtglttatacagctcagcttcttcttcttctgagagaacaa 1500
Qy 1498 TAAGACATTAAGGAAAGATTCATGTGATATTAAGATGGGACACTTGTCTTTCTT 1557
Db 1501 taagacataagggaaagatcatgtggaatataaaagaatgagcttgcacttcttctt 1560
Qy 1558 GACTCTTGTTCAGTTTCAATTCAGTGTCTGATGATGACAGACATTTTAAATGAAG 1617
Db 1561 gactcttgttctcagtttcaatcaatcagtgctgtactgtgacagacacttctaagaag 1620
Qy 1618 TGCAAATTTGATACATATGTAATATGACTCACTTTTCTTGCGATCAAAATTTACGTC 1677
Db 1621 tgc aaattgatacataatgataatgactcagcttcttctgacagataaatttcaagctc 1680
Qy 1678 GTCTTCTGTATATGTGAGAGTACACTCTTATAGAAGTTCAAAAAGTTACAGCTTCCT 1737
Db 1681 gtcttctgtataactgtgaggtacacactctataagaagttcaaaaagttcaagcttccct 1740
Qy 1738 TTCCTTTTCACTCAGTAAGTAATGGGGTCTGCTCAAGTCTGAAGAAGTCTATTGTGA 1797
Db 1741 tctcttctaactccaagtaagtaagtggtccgtcctcaagttgaagaagctcattttgca 1800
Qy 1798 CTGTAGCCTGCGCTGTGTAATGAGCAATCTATTTAACTGGCTTCAGGCTCCCCAC 1857
Db 1801 ctgtagcctgcgctgtgtaattgacacactctatttaactgtctcagctccccaac 1860

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Qy 1858 CTTCCTCAGCCACCTCTCTTTTTCAGTTGGCTGACTTCACACACAGATCATGAGTG 1917
Db 1861 ctctctcagccacactctcttcttcaagttggtgacttccacacactcagatctcatgagtg 1920
Qy 1918 CCAAGCAAAAGAGAGAGAGAGAAATAGCTGCGCGGTTTTTTTAAATTGGGGTTTTGC 1977
Db 1921 ccaagcaaaagagagagagaaatagcctgcgcggttctttagtttgggttttgc 1980
Qy 1978 TGTTCCTTTTATGAGACCATTCCTATTTCCTTATAGCAATGTTCTTTATACATA 2037
Db 1981 tgttcctttatgagaccatctcattcttctttagtccaatgttcttataacagata 2040
Qy 2038 TTATTATGTAAGAAACATCAGTGAATGCTAGCTGCAAGTGACATTCCTTTGATGATA 2097
Db 2041 ttattatgaagaaacaacactgaatgctagctgcgaagtgacatctctttagatgata 2100
Qy 2098 TSGAAGAGTTAAACAGGTGAGAAATTCCTTGATTTACAAATGAATGCTCTCTTCC 2157
Db 2101 tsgaagagttaaaacaagctggaataatccttgatccaatgaaatgctctcctcc 2160
Qy 2158 CTGCCCCAGAACTTTTATCCACTTACCTAGATTCATATTTCTTAAATTCATCTCA 2217
Db 2161 ctgccccagaaactttataccaacttacctagattctacatattccttaaatlcaatcca 2220
Qy 2218 GGCCTCCCTCAACCCCAAGGCGCGCCAGACACACTGGAATTC 2259
Db 2221 ggcctccctcaaccccaagggcgcgagacactggaattc 2262

RESULT 11
ID T14723 standard: cDNA: 2350 BP.
XX
AC T14723:
XX
DT 31-OCN-1996 (first entry)
XX
DE Human Leu8 antigen cDNA (major transcript).
XX
KW Cell surface antigen; cloning; immunoselection; immunotherapy;
therapy; diagnosis; vector; COS; Leu9; T-lymphocyte; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 50..1207
FT FT /tag= a
FT FT 1079..1514
FT FT /note= "bases 1079-1514 are deleted in the
shorter cDNA clone"
PN US5506126-A.
PD 09-APR-1996.
XX
PF 25-FEB-1988; 88US-0160416.
XX
PR 01-DEC-1992; 92US-0983647.
PR 25-FEB-1988; 88US-0160416.
PR 13-JUL-1989; 89US-0379076.
PR 13-JUL-1990; 90US-0553759.
PR 18-OCT-1993; 93US-0139273.
XX
PA (GENE) GEN HOSPITAL CORP.
PI Aruffo A, Seed B;
XX
DR WPI: 1996-200279/20.
DR P-PSDB: R91442.
XX
XX Cloning of cDNA encoding cell surface antigen - useful for isolation
PT

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QY	1902	TAGCATCTCATGAGAGTGGCCAAACAAAAGAGAGAGAAGAAATAGGCTGGCGGCTTTT	1961
Db	1863	tagcatctcatgagatgccaagcaaaagagagagaagaataagcctgcgtgttttt	1922
QY	1962	ACTTTGGGGGTTTGGTGGTTCCTTTTATGAGACCCATTCCATTTCCTTATAGTCATGT	2021
Db	1923	agcttggggggtttggcgtgttcccttataagaagccattccattctataagtaatgt	1982
QY	2022	TTGCTTTATTCACGATTAATATTAGTAAGAAACATCTACTGAAATGGTAGCTGCAAGTGACA	2081
Db	1983	ttcttatacagatattattatgaagaagaacaacatcgaataatgctagctgaagtaca	2042
QY	2082	TCTCTTATATGTCAATATGAGAGAGTTAAACACAGTGAGAGAAATTCCTTGATTCAATGA	2141
Db	2043	tctcttataatgcatatagaagaagtaaaacagtgagaaatccctgattcaacaatga	2102
QY	2142	AATGCTGCTCTTCCCTCCGCGCCACAGAACTTTATGC -ACTTACGTAGATTCTCATATT	2200
Db	2103	aatgcttccttccctccctgcccaagaccttataatccgacttaactaagattctacatat	2162
QY	2201	CTTTAAATTTTCATCTCAGGGCTCCCTCAACCCGAC	2235
Db	2163	ctttaaattcatctcagcctccccaacccac	2197
RESULT 12			
Q21184			
ID	Q21184	standard; DNA; 2350 BP.	
XX			
AC	Q21184;		
XX			
DT	21-MAY-1992	(first entry)	
XX			
DE	Encodes T lymphocyte-specific Leu8 Antigen major form.		
XX			
KW	Rapid immunoselection cloning technique; cell surface antigen;		
KW	homolog receptor; antigen-presenting cells; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	W09201049-A.		
XX			
XX			
PD	23-JAN-1992.		
XX			
PF	15-JUL-1990;	90WO-US04986.	
XX			
PR	13-JUL-1990;	90US-0553759.	
XX			
PA	(GEHO-) GEN HOSPITAL CORP.		
PI	Seed B, Aruffo A, Amiot M;		
XX			
DR	WPI: 1992-056864/07.		
DR	P-PSDB; R20815.		
XX			
PT	New CD53 cell surface antigen and DNA encoding it - for		
XX	immuno-therapy and diagnosis of haematopoietic neoplasms, etc.		
XX			
PS	Example 14: Page 106; 160pp; English.		
CC	Two CDNA clones encoding Leu8 determinants were isolated from a		
CC	human T cell library using the rapid immunoselection cloning method		
CC	(see e.g. Q21164 for description of method). The shorter insert		
CC	(see Q22500) lacks 436 internal residues (i.e. nucleotides 1079 to		
CC	1514 of the longer insert). RNA blot hybridisation		
CC	revealed a major transcript of 2.4kb in peripheral blood		
CC	mononuclear cells, tonsillar B cells and the Jurkat and HSB-2		
CC	leukemic T cell lines. A minor transcript of 2.0kb was present in		

CC peripheral blood mononuclear cells and the Jurkat and Hs α -2
CC leukaemic T cell lines. The protein encoded by the larger insert
CC is closely related to the murine Mel-14 homing receptor.
XX
SQ Sequence 2350 BP; 679 A; 519 C; 490 G; 662 T; 0 other;

50 Sequence 2350 BP; 679 A; 519 C; 490 G; 662 T; 0 other;

Query Match	94.1%;	Score 2126.2;	DB 13;	Length 2350;
Best Local Similarity	99.28;	Pred. No. 0;		
Matches 2178; Conservative	0;	Mismatches 13;	Indels 4;	Gaps 4

44 CCCTTGGCAAGACCTGAGACCTTGTCTAAGTCAAGAGGCTCAATGGGCTGCAGAG 103

Db 4 ccttggcgaagcaccgagacccttgctgaagtcagaagctcaatggctgcagaag 63

QY 104 AACTAGAGAAAGACCACCAAGCCATATTTTCCATGTGAAATGTGACAGCACCACGAG 163
|||||
Db 64 AACTAGAGAAAGACCACCAAGCCATATTTTCCATGTGAAATGTGACAGCACCACGAG 123
|||||

164 GGACTTATGGACATCTTCAGTTGTGGGGGTGACATGCTCTGTGTGATTTCCTGGC 223

Db 124 ggacttataacatcttcaagltgtggggtggacaatgctctgtgtgatttcctgac 183

QY 224 ACATCATGGAACTACTGCTGGACTTACCATTTATTTGTAAAAAACCATGAAGCTGGCAAG 283

UU acatcatcggaaacgcgaactgcgcggaacttaaccattatctctgtaaaaaaacccatgaaactgcgcaag 243
 QY 184 ggcctagaaagattcmgcccgaagacaatttacacagattttagttgccattacaaaaaaccaaggcga 343
 284 ggcctagaaagattcmgcccgaagacaatttacacagattttagttgccattacaaaaaaccaaggcga 343

Db 244 ggc tagaagatctctgcgagacaattacacagattagtgtgcataacaacagcgga 303

344 AATTAGTATCTGGAGAAGACTCTGCCCTCAGTCGTCTTACTACTGGATAGGAATCCG 403

Db 304 aattgagtatctcygagaagactctgcctttcagtcgttcttactactygaatgcg 363

Dbb 364 gaagataggaagataatgaacgttgggttggaaccacaacatctctcaatgaaagacaga 423

464 GAACTGGGAGATGTTGAGCCCAACACACAGAAGAACAAGAGAGACTGCTGGAGATCTTA 523

Db 424 gaactggggagatgtgtagcccaacaacaagaagaacaagagagactgcgttgagatcca 483

0y 524 TATCAGAGAAACAAGATGCAGCCAAATGCAGATGATCGCTGCCACAACTAAAGGC 583
 484 TATCAGAGAAACAAGATGTCAGCCAAATGCAGATGATCGCTGCCACAACTAAAGGC 543

584 AGCCCTCTGTTACACAGCTTCTTGCCAGCCCTGGTCATGCAGTGGCCATGGAGATGTGT 643

Db 544 agccctctgtacacacagctctctgccagccctgtgcatcatgacagtgaggaatgtgt 603

644 AGAATCATCATTAATACACACCTGCAACTGTGATGTGGCTACTATGGGCCCACTTCA 703

D0 604 agaaatcatcataattacacctgaactgtgltgtgggttactatgtgccccagtlca 663

OY 704 GCCTTGATTCAGTGTGACCCCTTTGGAGGCCCCAGAGCTGGGTACCATGGACTTACTTCA 763

Db 664 gttctgattccagtgtagcccttggagagcccccagagctggtgatactgtaattaccca 723

QY 764 CCCCTTGGAACTTCAGCTCAGCTCACAGTGTGCTTCAGCTGCTCTGAAAGMACAA 823

Db 724 ctctcttggaacttcagcttcagctcacagtgctgcttcagcgtctgaagaacaa 783

Accession	Sequence	Position
024	CTTACCTGGATTGGAAGAACCTACCTGTGGACCATTTTGGAACTGGTCATCTCCGAAC	883
D8784	CTTAACGTGATLTGAAGAACCACTGTGGACCATTTGAACTGTGTCATCTCCGAAC	843

QY 884 AACCTGTAAGTATTCAGTGTGAGCCCTATACAGCAACAGATTGGGGATCATGAACGTG 943

Db 844 aaactgtcaagtgtatctacgtgtgagccctctatcagcaccagatcttgggatcatgaactg 903

QY 944 TACCATCCCCGACAGCTTACGCTTGCATGTACTTCACTCATCTGCTCAGAAAG 1003
|||||

[illegible]

Oy	2142	AATGCTCTCTCCCTTCCCCTGGCCCCAACAACCTTTATTCG-ACCTACTAGATTCTCATATTT	2200
Db	2103	aatgcctcctccctccctgcccccaagactttatccgaacttaacataattcatat	2162
Oy	2201	CCTTAATAATTCAATCTCAGCGCTCCCTCAACGCCAC	2235
Db	2163	ccttaaatccaatcacaggacctcccaaccacaac	2197
RESULT 14			
ID	V81217		
XX	V81217 standard: cDNA; 2350 BP.		
AC			
XX	V81217:		
XX			
DT	10-MAY-1999 (first entry)		
XX			
DE	Human Leu8 antigen cDNA.		
XX			
KW	Leu8; cell surface antigen; human; T lymphocyte; cDNA library;		
RW	ss.		
XX			
OS	Homo sapiens.		
XX			
FH		Location/Qualifiers	
FT	Key	50..1207	
FT	CDS	/*tag= a	
XX			
PN	US5849898-A.		
XX			
PD	15-DEC-1998.		
XX			
FE	07-JUN-1995; 95US-0485447.		
XX			
PR	01-DEC-1992; 92US-0983647.		
PR	25-FEB-1988; 88US-0160416.		
PR	13-JUL-1989; 89US-0379076.		
PR	23-MAR-1990; 90US-0498809.		
PR	13-JUL-1990; 90US-0553759.		
PR	07-JUN-1995; 95US-0485447.		
XX			
PA	(GEHO) GEN HOSPITAL CORP.		
PI			
PI	Allen J., Amiot M., Aruffo A., Camerini D., Laufer L,		
PI	Quendo C, Seed B, Simmons D, Stamenkovic I, Stengelin S;		
XX			
DR	WPI; 1999-069813/20.		
XX	P-PDB: W86199.		
PT			
PT	cDNA encoding human CD40 antigen - useful for cloning cDNA encoding		
PT	cell surface antigens; constructing cDNA libraries; expression		
PT	vectors for expression in eukaryotic cells or their fragments		
XX			
XX	Example 14; Column 67-70; 79pp; English.		
CC			
CC	This nucleotide sequence comprises human Leu8 cDNA. The cDNA was		
CC	isolated from a human T lymphocyte cDNA library using a novel		
CC	method for cloning cDNAs from mammalian expression libraries. The		
CC	method is based on transient expression of an antigen in eukaryotic		
CC	cells and physical selection of cells expressing the antigen by		
CC	adhesion to an antibody-coated substrate. The method is useful for		
CC	the isolation and molecular cloning of any protein which can be		
CC	expressed and transported to the cell surface membrane of a		
CC	eukaryotic cell. It has been used to clone genes (see V81198-220)		
CC	encoding cell surface antigens such as CD1a, CD1b, CD1c, CD2, CD6,		
CC	CD7, CD13, CD14, CD16, CD19, CD20, CD22, CD26, CD27, CD28, CD31,		
CC	CDw32a, CDw32b, CD33, CD34, CD36, CD37, CD38, CD39, CD40, CD43,		
CC	CD44, CD53, ICAM, LFA-3, FCRIIa, FERIt, TLISa and Leu8 (see		
CC	W86188-62, W89151-52 and W86451).		
CC	Specifically claimed. Leu8, a T lymphocyte antigen, has been		
CC	expressed in COS cells.		
XX			

Query Match	94.1%;	Score 2126.2;	DB 20;	Length 2350;
Best Local Similarity	99.2%;	Pred. No. 0;		
Matches 2178;	Conservative 0;	Mismatches 13;	Indels 4;	Gaps 4;
44	CCCTTTGGCAAGGAGCCTTGAGACCCCTTGTCTTAAGTCAAGAGAGGCTCAATGGCTGCAGAG	103		
4	cccttgggcaaggagcccttgagaccctcttgctaaagccaagggctcaatcagctcgtgaagag	63		
104	AACCTAGACAGAGCAACCAAGCCATGATATTTCCATGGAATGTCAAGACCCACAG	163		
64	aactagagagagccaaagcaaaagccatgatattccatgynaatgctcagagcaaccagag	123		
164	GGACTTATGGAACATCTTCAAGTTGTGGGGGGGAGCAATGGCTGTGATTTCTCTGGC	223		
124	ggaactatgynaacatcttcaagcttgctgggggagacaatgcccgtgctgcatctccggc	183		
224	ACATCATGGAACCTTACTGCTGGACTTACCATTATTTCTMAAAACCACATGCACTGGCAAG	283		
184	acatcatggaacccgactcgtgacttaccatattcttgaaaaaccatgaaactcgtcaag	243		
284	GGCTTGAAGATTCTGCCGAGACATTTACACAGATTTACTTGCCATACAAACAGCGCGA	343		
244	ggctagaagatctctcgagacaattacaagatttaagcttccatacaaaaagcgga	303		
344	AATTAGATCTGGGGAAGAGACTCCCTTCAGTGCCTTACTACTCTGATATGGAATCCG	403		
304	aattgagatctcgggaagaaactctgccttccatctgcttcttaactcgtgaatgaatccg	363		
404	GAAGATAGGAGGAATATGAGCGTGGGTGGGAACCAACAATCTCTCACTGGAAGAAGCAGA	463		
364	gaagatagaggaataatgagacgttgggaggaaacaaacaatctccactggaagaagcaga	423		
464	CAACTGGGGAGATGCTGAGCCCAACAACAAGAAGAACAGAGACTCTCGTGAGATCTTA	523		
424	gaactggggagatctgtgagcccaaaaagaagaagaagactcgtgagatcta	483		
524	TATCAAGGAAGAAACAAGATGCGAGCAATGGAACATGACGCTCCCAAACTMAAGC	583		
484	tatcaagagaaacaaagatcagagaatctgaaagaagaaagccctgcgccaacaaagagc	543		
584	AGCCCTCTGTTACACAGCTTCTTGGCAGCCCTGGTCAATGACAGTGGCCAATGGAGATTTGT	643		
544	agccctctgttaacagaagcttctgcagccctgcgtcactcgaagctcagtgaaatgct	603		
644	AGAATTCATTAATTCACACACTGCACTGTGATGTGGGTACTATATGGGCCCCAGTGTCA	703		
604	agaaatcatcaaatatcacactgcaacttgaatgttgggtactatgagcccgatgca	663		
704	GCTTGTGATTTAGTGTGAGGCTTTGGAGGCCCGAGAGTGGGTACCAATGAGACTGACTCA	763		
664	gcttgtgattcagtgtaggcctcttgagggcccgagatctggtatcacaagactgtactca	723		
764	CCCTTTGGAACCTTACACTTCAAGTCACTGTGACCTTTCAGCTTCTTGAAGAACA	823		
724	ctctcttggaaaactcagcttcagctcaagcttgcgtcttcagcgtctcttggaagaacaa	783		
824	CTTAACTGGGAATTGAGAACAACCACTGTGACCAATTTGGAACCTGTTCATCTCGAAGAC	883		
784	cttaactggaattgagaacaacaccttggagacatttggaactcgttcatctccgaagcc	843		
884	AACCTGTCAACTGATTTCAAGTGTGAGCCCTTTCAGACACCAATTTGGGGATCATGAATG	943		
844	aaacctgtcaagtgtatcagtgtagccctctatcagacacaaatcttgggatacagaaactg	903		
944	TAGCCATCCCTGGCCACACTTACGCTTACCTGTGACATGTACCTTTCATCTCTCAGAAG	1003		
904	tagccatccctcctgcagcttcagcttactcttcgcatgataccttcaatcctcgtcaagaag	963		
1004	AACCTGATTTAATTTGGGAAGAAACCAATTTGTTCATCATCTGCAATCTGGTCAAAATCC	1063		

Db	964	aacitgagftaatitgggaagaagaacacattitgtaatcatctggaatctgtgcaaatcc	1023
QY	1064	TAGTCAATATATGTCAAAAATTGGACMAAAGTTTCTCAATGATTAAGAGGGGTGATTAA	1123
Db	1024	taatccaataatgtaaaaatttgcacaaagtcttccaatgataaaggagggttgattataa	1083
QY	1124	CCCCCTCCTTCAATCCAGTGGAGGACATGATGCTTACGATTCCTCTGGGTTGGCATTTATCAT	1183
Db	1084	ccccctcatctccagtgaggagcaatggttaactgcattctctggtgttggaattatcat	1143
QY	1184	TTGGCTGGCAAGAGATTAAAAAAGCCAGMAAATCCAGAGAAAGTGTGAATGACCATA	1243
Db	1144	ttggctggaagaagattaaaaaaaggcaagaatccaaggagtaatgaatgaccata	1203
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QY	1304	TCCTTCATGAAACGTTTTGTGTGGGCACTCTTCAATGTCMAACATGAAGTGTG-TCGC	1362
Db	1264	tccttcgatgaacgcttctgt	1323
QY	1363	TTGATGCTATCTGGGAAGATTTCACCCGACCAACATTCCTCTCAGCTTTCATTTGGCCC	1422
Db	1324	ttcagtgacatctcgggaagattcttcaactgcacaaagcttcccttcacatcttcacatgcgc	1383
QY	1423	CTCATTTATCCCTMACCCCCAGCCGACAGTGTTTATACGCTCAAGCTTTTGTGCTTTT	1482
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QY	1483	CTGAGGAAACAATAATGAAGCAT- AAGGAAAGGATTCACTGTGAATATGAAGTGGCT	1541
Db	1444	ctgaggagaacaataaagaaccaataagggaagagattcatctggaataaagaatgagct	1503
QY	1542	GACTTGGCTCTTCTTGACCTCTGTGTTTCAGTTTCATTCAGTGGCTGACTGATGACAG	1601
Db	1504	gaacttggctcttcttgacctctgtttcaattcaatccagtgctgcgtacatgagagag	1563
QY	1602	ACACTTCTAAATGAAGTGCAAATTTATATGATATGTGAATATGAGACTGAGTTTCTTGA	1661
Db	1564	acacttctaataatgaatgacaaattatataatgtaataatgagactcagttctctgca	1623
QY	1662	GATCAAAATTTACAGTGTCTGCTGTATACGTCGAGCTCACCTTATGGAAGTTTCAA	1721
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QY	1722	AACTCAGCTCTCTCTTTCTTTCTTAACTCCAGTAAGTAATGGGGTCTGCTCAAGTTGA	1781
Db	1684	aactcagactctctcttcttcttctaactcagtgaaatggtgtccgtccagttga	1743
QY	1782	AAGAGTCTATTGGCATCTAGCTGTGGCGGTGTGGAATTTGACATCTTATTAATCTG	1841
Db	1744	aagagttcatttgcactgtgagccctgcgcgtctgtgaaatggaacatcatatctaacgtg	1803
QY	1842	CTTACAGGCTCCCACTCTTTCAGCACCTCTCTTTTTCAGTTGGCTACTTCCACACC	1901
Db	1804	cttca- gctccccaacctcttcagcaacctctcttlttcagttgtgcacttccaacc	1862
QY	1902	TGCAATCTATAGTGGCAAGCAAAAGAGAGAAAGAAATACCTGCGCGGTTTTT	1961
Db	1863	tggcatctcaatgagtgccaagaagaagagagaagaatagcctgcgcgtgttltt	1922
QY	1962	AGTTTGGGGGTTTCTGTTTCTTTTATGAGACCATTCATTTCTTATATGTCATG	2021
Db	1923	agtttggggggttctgttcttcttcttcttcttcttcttcttcttcttcttcttcttctt	1982
QY	2022	TTCCTTTATCAGATATTATTAGTAAAGAAATCATTGAAATGCTAGCTCAAGTGACA	2081
Db	1983	ttcttltatcaagatatattatagtaagaanaacatcaactgaaatgctagctgcaagtga	2042
QY	2082	TCTCTTATGATGATGGAAGAGTTAAACAGGGGGAATTCCTGATTCACATGA	2141
Db	2043	tctcttgaatgcatatgagaagfttaaaaaaagtgagggaatctccttgattccaatga	2102

QY	2142	ATATGCTGTCCTTTCCCGGCCCCGAGACTTTATGC-ACCTACCTAGATTTCACATATT	2200
QY	2103	aatgctctcccttccctgcgccagagccctttttatccgacttaacctaatataatt	2162
QY	2201	CTTTAAATTTATCTCAGAGCCTCCCTTAACCCAC	2235
Db	2163	cttataattcatctcagcctccctctaaacccac	2197

RESULT	15
Q71006	
ID	Q71006 standard; cDNA; 2330 BP.
XY	

AC Q71006;

DT 25-MAR-1995 (first entry)
 XY

DE L-selectin cDNA.

L-selectin; lectin domain; ligand-binding polypeptide; low-density lipoprotein receptor

KM post-reperfusion injury; organ/tissue transplant rejection;
inflammation; inhibition; platelet; mononuclear cell; tissue damage; autoimmune disease

KW	thrombosis; ss.
YX	

Homo sapiens.

FH Key

CDs	53.11210
E1	/*tag= a
ET	

FT
XY
/product= L-selectin

PN W09417193-A.

PD 04-AUG-1994.

AA 25-JAN-1994; 94WO-US00909

XX	25-JAN-1993.	93RIS-0008459
PR		

XX
XX
(NAME) DATE RECEIVED BY: _____

XX

XX

DR WPL: 1994-264106/32.
DR P-P\$DB: R56663.

Now bl f u e n c + i o e s l e t u m e n t i n g e n e r a t e s a n d a p p e a r s i n t h e a p p e n d i x e s .

selectin - and related DNA useful as leucocyte mobilising agent

PT also for targetted drug delivery.

PS Disclosure; Page 26-28; 56pp; English

This session concludes with a discussion of the implications of the findings for the design of future research and the development of interventions to improve the health and well-being of the population.

may be used in the construction of the new bifunctional ligand-

mobilising activity for treating tissue damage, autoimmune disease.

act by interfering with binding of leucocytes at the site of post-reperfusion injury or organ/tissue transplant rejection. They

inflammation and also inhibit platelet and mononuclear cell aggregation to prevent thrombosis.

bind to 2 different selectin ligands so provide more effective

XX compounds: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840

sequence 2330 BF; 001 A; 322 C; 48 / G; 660 I; 0 other;

[illegible]

Best Local Similarity 98.5%; Pred. No. 0;

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Dp	307	aattgatatcttgagaagaagccctgcctcttcagtcgtcttctaactgtgatagaaatccg	366
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Dp	727	ccctcttggaaacttcaacttcaacttcaacaaaggtgtgcttccagctgtctctgaagaaacaa	786
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Dp	967	aaactgtatctaatcttggaagaagaacaacatctgtgaatcatcttggaatctgttcaaatcc	1026
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OY	2022	TTCTTTTATCAGATATTTATTAGTAGAAMAACATCACTGAATGTAGCTGCAAGTGAACA	2081
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Search completed: January 13, 2001, 00:37:12
Job time: 16618 sec

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OM nucleic - nucleic search, using sw model

Run on: January 12, 2001, 16:24:14 : Search time 79.76 seconds
(without alignments)
4564.457 Million cell updates/sec

Title: US-09-119-209-1

Perfect score: 2259

Sequence: 1 GAATTCGACTGCTGCTGCTT.....CCGCACGACACTGGAATTC 2259

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0
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Listing first 45 summaries

Database : Issued_Patents_NA:*
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5: /cgn2_6/ptodata/2/lna/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2087.6	92.4	2330	1 US-08-481-803-1	Sequence 1, Appli
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4	2087.6	92.4	2330	1 US-08-340-539A-1	Sequence 1, Appli
5	2087.6	92.4	2330	2 US-08-461-592B-1	Sequence 1, Appli
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8	922.2	40.8	1696	2 US-08-461-592B-11	Sequence 11, Appli
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ALIGNMENTS

RESULT 1
US-08-513-278-1
Sequence 1, Application US/08513278
Patent No. 5840844
GENERAL INFORMATION:
APPLICANT: LASKY, LAURENCE A.
APPLICANT: STACHELL, SCOTT E.
APPLICANT: ROSEN, STEVEN D.
APPLICANT: SINGER, MARK S.
APPLICANT: YEDNICK, TED A.
TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patlin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513.278
FILING DATE: 10-AUG-1995
CLASSIFICATION: 5530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/059027
FILING DATE: 06-MAY-1993
APPLICATION NUMBER: 07/786149
FILING DATE: 31-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/315015
FILING DATE: 23-FEB-1989
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 33,055
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2259 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-513-278-1

Query Match	100.0%;	Score 2259;	DB 2;	Length 2259;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2259;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Db	661	ACACCTGCACACTGTGATGGGGTACTATGAGGCGCCAGTGCAGCTTGATTCACATGTG	720
Qy	721	AGCCTTTGGAGGCCCCAGAGTGGGTTACATGACATGTACTACCCCTTTGGAAACTTCA	780
Db	721	AGCCTTTGGAGGCCCCAGAGTGGGTTACATGACATGTACTACCCCTTTGGAAACTTCA	780
Qy	781	GCTTCAGCTCAGATGTGCTTCAGCTGCTCTAAGAACAAACTTAAGTGGATTTGAAG	840
Db	781	GCTTCAGCTCAGATGTGCTTCAGCTGCTCTAAGAACAAACTTAAGTGGATTTGAAG	840
Qy	841	AAACCACTGTGGACCAATTTTGGAACTGGTTCATCTCCAGAACCAACTGTCAAGTATTC	900
Db	841	AAACCACTGTGGACCAATTTTGGAACTGGTTCATCTCCAGAACCAACTGTCAAGTATTC	900
Qy	901	AGTGTGAGCCCTCTATTCAGACACAGATTTGGGGATCTCAAGTGTGACATCCCTGGGCA	960
Db	901	AGTGTGAGCCCTCTATTCAGACACAGATTTGGGGATCTCAAGTGTGACATCCCTGGGCA	960
Qy	961	GCTTCACCTTACTCTCTGCACTGTACCTTATCTGCTCAGAGGAACCTAGATTAAATGGGA	1020
Db	961	GCTTCACCTTACTCTCTGCACTGTACCTTATCTGCTCAGAGGAACCTAGATTAAATGGGA	1020

Qy	1021	AGAGAAACCATTTTGATATATCGAAATGTGTCACAAATGCTAGTCCATATGTCAA	1080
Db	1021	AGAGAAACCATTTTGATATATCGAAATGTGTCACAAATGCTAGTCCATATGTCAA	1080
Qy	1081	AATTTGCAAAAGTTTCTAATGATTAGAGGGGTGATTTAAACCCGCTTCATTCCAG	1140
Db	1081	AATTTGCAAAAGTTTCTAATGATTAGAGGGGTGATTTAAACCCGCTTCATTCCAG	1140
Qy	1141	TGCGAGTCATGGTTACTGTCAATTCCTGGGTTGGCATTTATCTTGGCGGCAAGAGAT	1200
Db	1141	TGCGAGTCATGGTTACTGTCAATTCCTGGGTTGGCATTTATCATTTGGCGGCAAGAGAT	1200
Qy	1201	TAAAAAAGGCAAGAAATCCAAAGAAAGTATGAAATGACCCATTTAATTCGCGCTTGGTG	1260
Db	1201	TAAAAAAGGCAAGAAATCCAAAGAAAGTATGAAATGACCCATTTAATTCGCGCTTGGTG	1260
Qy	1261	AAAGAAATTTCTTGGAATACTAAAAATCATAGACATCCTTTAAATCCTTCATGAAAGTT	1320
Db	1261	AAAGAAATTTCTTGGAATACTAAAAATCATAGACATCCTTTAAATCCTTCATGAAAGTT	1320
Qy	1321	TTGTGGTGGGACCTCCTACGTAAACATGAAGTGTTCCTTATGTCAATCTGGGAAG	1380
Db	1321	TTGTGGTGGGACCTCCTACGTAAACATGAAGTGTTCCTTATGTCAATCTGGGAAG	1380
Qy	1381	ATTTTACCCGACACAGAGTTCCTTCAGTTCATTTCCGCCCTCATTTATCCCTCAAC	1440
Db	1381	ATTTTACCCGACACAGAGTTCCTTCAGTTCATTTCCGCCCTCATTTATTCCTCAAC	1440
Qy	1441	CCGAGCCCAAGGTGTTTATACAGCTCACTTTTGTCTTTTCTGAGAGAAACAATAA	1500
Db	1441	CCGAGCCCAAGGTGTTTATACAGCTCACTTTTGTCTTTTCTGAGAGAAACAATAA	1500
Qy	1501	GACCAATTAAGGGAAGAGATTCATGTGGAAATATAAGTGGCTGACCTTCCTTCAGAC	1560
Db	1501	GACCAATTAAGGGAAGAGATTCATGTGGAAATATAAGTGGCTGACCTTCCTTCAGAC	1560
Qy	1561	TCCTTGTTCAGTTTCAATTCAGTGTCTGATCTGTGATGACAGACATTCCTAAATGAATGC	1620
Db	1561	TCCTTGTTCAGTTTCAATTCAGTGTCTGATCTGTGATGACAGACATTCCTAAATGAATGC	1620
Qy	1621	AAATTTGATATCTGTGAATATGAGCATGATTTCTTGAGATCAATTTCACTGCTGTC	1680
Db	1621	AAATTTGATATCTGTGAATATGAGCATGATTTCTTGAGATCAATTTCACTGCTGTC	1680
Qy	1681	TTCTGTATATCTGTGAGAGTACACTCTTATATAGAAATTCGAAAAGCTACGCTCCCTTC	1740
Db	1681	TTCTGTATATCTGTGAGAGTACACTCTTATATAGAAATTCGAAAAGCTACGCTCCCTTC	1740
Qy	1741	TTTTCTAACTCCAGTGAAGTATGGGGTCTGCTCAAGTTGAAGAAGTCAATTTGGCAGTG	1800
Db	1741	TTTTCTAACTCCAGTGAAGTATGGGGTCTGCTCAAGTTGAAGAAGTCAATTTGGCAGTG	1800
Qy	1801	TAGCCTCGCCGTCTGTGAATTTGGACATCTTTAATCGGCTTCAGGCTCCCCACCTT	1860
Db	1801	TAGCCTCGCCGTCTGTGAATTTGGACATCTTTAATCGGCTTCAGGCTCCCCACCTT	1860
Qy	1861	CTTCAGCCACCTCTTTTTCAGTTGGCTGCACTTCCACACTTACATCTCATGAGTGCCA	1920
Db	1861	CTTCAGCCACCTCTTTTTCAGTTGGCTGCACTTCCACACTTACATCTCATGAGTGCCA	1920
Qy	1921	AGCAAAAGGAGAAAGAAATAGCCTGCGCGGTTTTTTAGTTTGGGGGTTTTGCTGT	1980
Db	1921	AGCAAAAGGAGAAAGAAATAGCCTGCGCGGTTTTTTAGTTTGGGGGTTTTGCTGT	1980
Qy	1981	TTCTTTTATGAGACCATTCCTATTTCTTATATGATGTTCTTTTATACAGATATTA	2040
Db	1981	TTCTTTTATGAGACCATTCCTATTTCTTATATGATGTTCTTTTATACAGATATTA	2040
Qy	2041	TTAGTAAAGAAACATCTGAAATGCTAGTGAAGTGAACATCTCTTTGATGTCAATAGG	2100
Db	2041	TTAGTAAAGAAACATCTGAAATGCTAGTGAAGTGAACATCTCTTTGATGTCAATAGG	2100

Qy	2101	AAGGTTAAAAACAGGAGAAATTCCTTGATTCACAATGAAGAACTCTCCCTTCCCTG	2160
Qy <td>2101 <td>AAGGTTAAAAACAGGAGAAATTCCTTGATTCACAATGAAGAACTCTCCCTTCCCTG <td>2160</td> </td></td>	2101 <td>AAGGTTAAAAACAGGAGAAATTCCTTGATTCACAATGAAGAACTCTCCCTTCCCTG <td>2160</td> </td>	AAGGTTAAAAACAGGAGAAATTCCTTGATTCACAATGAAGAACTCTCCCTTCCCTG <td>2160</td>	2160
Db <td>2101 <td>AAGGTTAAAAACAGGTCGAGAAATTCCTTGATTCACAAGAAATCTCTCCCTTCCCTG <td>2160</td> </td></td>	2101 <td>AAGGTTAAAAACAGGTCGAGAAATTCCTTGATTCACAAGAAATCTCTCCCTTCCCTG <td>2160</td> </td>	AAGGTTAAAAACAGGTCGAGAAATTCCTTGATTCACAAGAAATCTCTCCCTTCCCTG <td>2160</td>	2160
Qy <td>2161 <td>CCCCCAGACCTTATTATCCACTTACAGATATTCACATATTCCTTAAATTTATCTCAGCG <td>2220</td> </td></td>	2161 <td>CCCCCAGACCTTATTATCCACTTACAGATATTCACATATTCCTTAAATTTATCTCAGCG <td>2220</td> </td>	CCCCCAGACCTTATTATCCACTTACAGATATTCACATATTCCTTAAATTTATCTCAGCG <td>2220</td>	2220
Db <td>2161 <td>CCCCCAGACCTTATTATCCACTTACAGATATTCACATATTCCTTAAATTTATCTCAGCG <td>2220</td> </td></td>	2161 <td>CCCCCAGACCTTATTATCCACTTACAGATATTCACATATTCCTTAAATTTATCTCAGCG <td>2220</td> </td>	CCCCCAGACCTTATTATCCACTTACAGATATTCACATATTCCTTAAATTTATCTCAGCG <td>2220</td>	2220
Qy <td>2221 <td>CTCCCTCAACCCACAGGAGCGCGCAGACACACAGGAATTC <td>2259</td> </td></td>	2221 <td>CTCCCTCAACCCACAGGAGCGCGCAGACACACAGGAATTC <td>2259</td> </td>	CTCCCTCAACCCACAGGAGCGCGCAGACACACAGGAATTC <td>2259</td>	2259
Db <td>2221 <td>CTCCCTCAACCCACAGGAGCGCGCAGACACACAGGAATTC</td> <td>2259</td> </td>	2221 <td>CTCCCTCAACCCACAGGAGCGCGCAGACACACAGGAATTC</td> <td>2259</td>	CTCCCTCAACCCACAGGAGCGCGCAGACACACAGGAATTC	2259

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RESULT 2
US-08-481-803-1
Sequence 1, Application US/08481803
Patent No. 5679346
GENERAL INFORMATION:
APPLICANT: Tedder, Thomas F. and Olivier G. Sperlini
TITLE OF INVENTION: MONOCLONAL ANTIBODY TO LYMPHOCYTE-ASSOCIATED CELL
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,803
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,366
FILING DATE: 21-MAR-1994
APPLICATION NUMBER: US 07/720,602
FILING DATE: 25-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/313,109
FILING DATE: 21-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: CG-101 CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX:
INFORMATION FOR SEQ. ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2330 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 53..1210
US-08-481-803-1

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Query Match	92.48;	Score 2087.6;	DB 1;	Length 2330;
Best Local Similarity	98.58;	Pred. No. 0;		
Matches 2161;	Conservative	0;	Mismatches 24;	Indels 9;
				Gaps 5

OY	44	CCCTTTGGCAAGGACCTTAGACCCCTTGCTGCTAAGCTCAAGAGGCTCATGTGGGCTGCAGAC	103
Db	7	CCTTTGGGCAAGACCTTAGACCCCTTGCTGCTAAGCTCAAGAGGCTCATGTGGGCTGCAGAC	66
OY	104	AACTAGAGAGGACCAACCAAGCCATGATATTTTCCATGTGCAATGTTCAGACACCCAGAC	153
Db	67	AACTAGAGAGAGGACCAACCAAGCCATGATATTTTCCATGTGCAATGTTCAGACACCCAGAC	126
OY	184	GGACTTATGGAACATCTTCAAGTTGTGGGGGTGCACAATGCTCTGTGTTGCAATTTTCC	223
Db	127	GGACTTATGGAACATCTTCAAGTTGTGGGGGTGCACAATGCTCTGTGTTGCAATTTTCC	186
OY	224	ACATCATGGAACCTACGCTGCTGGACTTCCATTTATTCGAAAAACCCATGAACTGGCAAG	283
Db	187	ACATCATGGAACCTACGCTGCTGGACTTCCATTTATTCGAAAAACCCATGAACTGGCAAG	246
OY	284	GGCTTGAAGATTTCTGGCCGAGACAAATTTACACAGATTTTAGTTGCCATACAAAAACAAGCCGA	343
Db	247	GGCTTGAAGATTTCTGGCCGAGACAAATTTACACAGATTTTAGTTGCCATACAAAAACAAGCCGA	306
OY	344	AATTGAGTATCTGGAGAAGACTCTGCCCTTTCAGTCTGTTCTTACTACTGGATAGGAATCCG	403
Db	307	AATTGAGTATCTGGAGAAGACTCTGCCCTTTCAGTCTGTTCTTACTACTGGATAGGAATCCG	366
OY	404	GAAAGTTAGSAGGAATTTGSGAGSTGGGTGGGAGCAACAAATCTCTCACTGAAAGAGAGA	463
Db	367	GAAAGTTAGSAGGAATTTGSGAGSTGGGTGGGAGCAACAAATCTCTCACTGAAAGAGAGA	426
OY	464	GAACGTGGGAGATGTTGTGAGCCCAACAAAGAAAGCAAGAGAGACTGCGTGGAGATCTA	523
Db	427	GAACGTGGGAGATGTTGTGAGCCCAACAAAGAAAGCAAGAGAGACTGCGTGGAGATCTA	486
OY	524	TATCAAGAGAAACAAGATGCGAGCCAAATGGAAACGATAGCGCTTCCACAACTAAAGGC	583
Db	487	TATCAAGAGAAACAAGATGCGAGCCAAATGGAAACGATAGCGCTTCCACAACTAAAGGC	546
OY	584	AGCCCTCTGTTACACAGCTTTTCCGACCCCTGGTTCATGCAGTGTGGCATGTGAGAAATGTGT	643
Db	547	AGCCCTCTGTTACACAGCTTTTCCGACCCCTGGTTCATGCAGTGTGGCATGTGAGAAATGTGT	606
OY	644	AGAAATCTCATATATCAACACCTGCACTGTGATGTGGGGACTATGSGGCCCAAGTGTCA	703
Db	607	AGAAATCTCATATATTAATTAACACTGCACTGTGATGTGGGGACTATGSGGCCCAAGTGTCA	666
OY	704	GCATTGTGATTCAGTGTGAGGCTTTTGGAGGGCCCAAGAGCTGGGTACCATGTGACTGTACTCA	763
Db	667	GCATTGTGATTCAGTGTGAGGCTTTTGGAGGGCCCAAGAGCTGGGTACCATGTGACTGTACTCA	726
OY	764	CCCCCTTGGAAACTTTCAGCTTCAGCTCAACAGTGTGCTTCAAGCTGCTCTGAAAGAACAA	823
Db	727	CCCCCTTGGAAACTTTCAGCTTCAGCTTCAGCTTCAAGCTGCTCTGAAAGAACAA	786
OY	824	CTTTAACTGGGATTTGAGAAACACACTGTGGAGCCATTTTGGAAACGTGCATCTGCAGAAC	883
Db	787	CTTTAACTGGGATTTGAGAAACACACTGTGCACATTTTGGAAACGTGCATCTGCAGAAC	846
OY	884	AACCTGTCAACTGATTCAGTGTGAGCCTCTATACGACACACAGATTTTGGGATTCATGAACTG	943
Db	847	AACCTGTCAACTGATTCAGTGTGAGCCTCTATACGACACACAGATTTTGGGATTCATGAACTG	906
OY	944	TAGCCATCCCTGGCCAGACTTCAGCTTACCTGTGCATGTACCTTCACTGTCTGCAGAAAG	1000
Db	907	TAGCCATCCCTGGCCAGACTTCAGCTTACCTGTGCATGTACCTTCACTGTCTGCAGAAAG	966
OY	1004	AACGTAGATTTATTTGGGAAGAAAGAACCATTTGTGATTCATCTGGAATCTGGCTCAATCC	1062
Db	967	AACGTAGATTTATTTGGGAAGAAAGAACCATTTGTGATTCATCTGGAATCTGGCTCAATCC	1022
OY	1064	TAGTTCATATATGTCAAAAAATTTGGACAAGATTTTCTCAATATATTAAGGAGCGCTATTTAA	1122
Db	1027	TAGTTCATATATGTCAAAAAATTTGGACAAGATTTTCTCAATATATTAAGGAGCGCTATTTAA	1088
OY	1124	CCCCCTTTCATTCACAGTGGCAGTCAATGTTACTGCAATTCCTGTGGGTTGGCATTTATCAT	1188

Accession	Sequence	Length
Db	1027 TAGTCATATGCTAAAAATTTGGCAAAAGCTTTCTCAATGATTAAAGAGCGTGATTATAA	108
Oy	1124 CCCCCCTCTTCATTCCAGTGGCAGTCATGTTACTGCATTTCTGCGGTTGGCATTTATCAT	118


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: NUMBER OF SEQUENCES: 28
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FISH & NEAVE
: STREET: 1251 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10020
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/340,539A
: FILING DATE: 16-NOV-1994
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/008,459
: FILING DATE: 25-JAN-1993
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Gunnison, Jane
: REGISTRATION NUMBER: 38,479
: REFERENCE/DOCKET NUMBER: CG-104 CON
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-596-9000
: TELEFAX: 212-596-9090
: INFORMATION FOR SEQ. ID NO: 1:
:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2330 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: MOLECULE TYPE: cDNA
:
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 53..1207
: US-08-340-539A-1

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Query Match          92.4%; Score 2087.6; DB 1; Length 2330;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 2161; Conservative 0; Mismatches 24; Indels 9; Gaps 5;

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QY 44 CCCCTTGGCAAGGAGCTGGAGCCCTTGTGCTAAGTCAGAGGCTCAATGGGCTGCAGAG 103
DB 7 CCTTTGGGCAAGGAGCTGGAGCCCTTGTGCTAAGTCAGAGGCTCAATGGGCTGCAGAG 66
QY 104 AACTGAGAGAGGAGCAAGCAAAAGCCATGATATTTCCATGGAATGTGAGAGCCAGAG 163
DB 67 AACTGAGAGAGGAGCAAGCAAAAGCCATGATATTTCCATGGAATGTGAGAGCCAGAG 126
QY 164 GGACTTATGGAACATCTCAAGTTGTGGGGTGGAGCAATGCTGTGTTGTGATTTCTGGC 223
DB 127 GGACTTATGGAACATCTCAAGTTGTGGGGTGGAGCAATGCTGTGTTGTGATTTCTGGC 186
QY 224 ACATCATGGAACCTAGCTGCTGACCTTACCATTTATTTGAAAAACCCATGAACTGGCAAG 283
DB 187 ACATCATGGAACCTAGCTGCTGACCTTACCATTTATTTGAAAAACCCATGAACTGGCAAG 246
QY 284 GGCTAGAAGATTTTGGCGAGACATTTACAGATTTAGTTGCCATACAAAACAAAGGCGA 343
DB 247 GGCTAGAAGATTTTGGCGAGACATTTACAGATTTAGTTGCCATACAAAACAAAGGCGA 306
QY 344 AATTGAGTATCTGGAGAAGACTGCGCTTCAGTCTGTTTACTACAGGATAGGAATCCG 403
DB 307 AATTGAGTATCTGGAGAAGACTGCGCTTCAGTCTGTTTACTACAGGATAGGAATCCG 366
QY 404 GAAGATTTGGAGGAATATGACGTGGGTGGAGCAACAAATCTCTGACGTAAGAGCAGA 463
DB 367 GAAGATTTGGAGGAATATGACGTGGGTGGAGCAACAAATCTCTGACGTAAGAGCAGA 426
QY 464 GAATGGGAGATGTGTGAGCCCAACAAAGAAAGAAAGAGGAGACTGGGTGAGATCTA 523

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DB 427 GAACCTGGGAGATGTGAGCCCAACAAAGAAAGAGGAGACTGCTGGAGATCTA 486
QY 524 TATCAGAGAAAACAAAGATGCGAGCAATGTGAGAGCATACCCCTGCCCAACAACTAAAGGC 583
DB 487 TATCAGAGAAAACAAAGATGCGAGCAATGTGAGAGCATACCCCTGCCCAACAACTAAAGGC 546
QY 584 AGCCCTGTGTACAGAGCTTCTTGGCAGCCCTGCGATGACAGTGGCCATGGAGAAATGTG 643
DB 547 AGCCCTGTGTACAGAGCTTCTTGGCAGCCCTGCGATGACAGTGGCCATGGAGAAATGTG 606
QY 644 AGAATATCATATATATTCACACCTGCACTGTGATGTGGGTACTATGAGGCCAGTGTCA 703
DB 607 AGAATATCATATATATATTCACACCTGCACTGTGATGTGGGTACTATGAGGCCAGTGTCA 666
QY 704 GCTTGTGATAGTGTGAGCCCTTGGAGGCCCGAGACTGGTACCATGTGACTGTACTCA 763
DB 667 GTTGTGATGATGATGTGAGCCCTTGGAGGCCCGAGACTGGTACCATGTGACTGTACTCA 726
QY 764 CCCCTTGGAAACTTCACCTTCACCTCAGAGTGTGCCCTTCAGCTGCTGTAAGAACAA 823
DB 727 CCCCTTGGAAACTTCACCTTCACCTCAGAGTGTGCCCTTCAGCTGCTGTAAGAACAA 786
QY 824 CTTAAGTGGATTAAGAAAACCACTGTGAGACATTTGGAACCTGTCTCAGAAC 883
DB 787 CTTAAGTGGATTAAGAAAACCACTGTGAGACATTTGGAACCTGTCTCAGAAC 846
QY 884 AACCTGTCACTGATTCAGTGTGAGCCCTTCATGAGCAGCAGATTTGGAGATCATGAACG 943
DB 847 AACCTGTCACTGATTCAGTGTGAGCCCTTCATGAGCAGCAGATTTGGAGATCATGAACG 906
QY 944 TAGCCATCCCTGGCCAGCTTCAGCTTACTCTGATGATGATGATGATGATGATGATGATG 1003
DB 907 TAGCCATCCCTGGCCAGCTTCAGCTTACTCTGATGATGATGATGATGATGATGATGATG 966
QY 1004 AACTGATTAATTGGGAAGAAACCAATTTGTGAATATCTGGAAATGCTCAAAATCC 1063
DB 967 AACTGATTAATTGGGAAGAAACCAATTTGTGAATATCTGGAAATGCTCAAAATCC 1026
QY 1064 TATGCCAATATGTCAAAAATTTGGCAAAAATTTGCAATGATTAAGAGGATGATTAATA 1123
DB 1027 TATGCCAATATGTCAAAAATTTGGCAAAAATTTGCAATGATTAAGAGGATGATTAATA 1086
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DB 1207 TTAATATGCGCCTTGGGAAGAAATTTCTGGAATATCTAATTAATTAATTAATTAATTA 1266
QY 1304 TCCCTTCATGAAGAGCTTTTGTGTGTGTGAGCAGCTCTGCAATCATGAAGTGTG-ATTCC 1362
DB 1267 TCCCTTCATGAAGAGCTTTTGTGTGTGTGAGCAGCTCTGCAATCATGAAGTGTG-ATTCC 1326
QY 1363 TTCAGTGCATCGGGAAGAAATTTTACCGGACCAACAGTTCCTTCAAGTTCATTTGCCCC 1422
DB 1327 TTCAGTGCATCGGGAAGAAATTTTACCGGACCAACAGTTCCTTCAAGTTCATTTGCCCC 1386
QY 1423 CTCATTTATCCCTCAACCCAGCCAGAGTGTGTTTATACAGGCAAGCTTTGTTGCTTTT 1482
DB 1387 CTCATTTATCCCTCAACCCAGCCAGAGTGTGTTTATACAGGCAAGCTTTGTTGCTTTT 1446
QY 1483 CTGAGGAGAAAACAAATTAAGACCAT-AAAGGAAGAGATTCATGTAATTAATTAAGATGCGT 1541
DB 1447 CTGAGGAGAAAACAAATTAAGACCATTAAGGAAGAGATTCATGTAATTAATTAAGATGCGT 1506
QY 1542 GACTTGTCTTTCTGATGCTGTGTTTTCAGTTTCAATTAAGTGTGATGATGATGATGATG 1601

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Db 1507 GACITTCGCTTTCCTTGAGCCTCGTTTTCAGTTTAATTCAGTGTGTAATTGATGACAG 1566
Qy 1602 ACACITTCATAATGAAGCAAAATTTATATCATATGTGAATATAGACTAGTTTTCTTGCA 1661
Db 1567 ACACITTCATAATGAAGCAAAATTTATATCATATGTGAATATAGACTAGTTTTCTTGCA 1626
Qy 1662 GATCAAATTTACAGTGTGCTCTGTGTATACGTGGAGAGTACACTCTTATAGAAGTTCCAA 1721
Db 1627 GATCAAATTTTCGGCTGTCTCTGTGTATAC- GTGGAGAGTACACTCT-- ---- ATGAAGTCAA 1680
Qy 1722 AAGTCACGCTCTCTCTCTCTCTAATCTACAGTGAAGTAAATGGGCTCCTGCACAAGTTGA 1781
Db 1681 AAGTCACGCTCTCTCTCTCTCTAATCTACAGTGAAGTAAATGGGCTCCTGCACAAGTTGA 1740
Qy 1782 AAGAGTCCTATTTTGCACTGTAGCTTCGCCGCTGTGTGAATTTGACCATCTTATTTACTGG 1841
Db 1741 AAGAGTCCTATTTTGCACTGTAGCTTCGCCGCTGTGTGAATTTGACCATCTTATTTAACGCG 1800
Qy 1842 CTTGAGGCGCTCCGCCACCTCTCTACAGCACCTCTCTTTTTCAAGTGGCTGCACCTCCACACC 1901
Db 1801 CTTCGA-GCCCTCCCCACCTCTCTACAGCACCTCTCTTTTTCAAGTGGCTGCACCTCCACACC 1859
Qy 1902 TAGACATCTATGAGTGCACCAAGCAAAAGAGAGAAGAAATFACCTGCSCGGCTTTTTT 1961
Db 1860 TAGACATCTATGAGTGCACCAAGCAAAAGAGAGAAGAAATFACCTGCSCGGCTTTTTT 1919
Qy 1962 AGTTTTGGGGCTTTTGGCTGTTCCTTTTTATGAGACCACATTCCTAATTTCTTATAGTCAATGT 2021
Db 1920 AGTTTTGGGGCTTTTGGCTGTTCCTTTTTATGAGACCACATTCCTAATTTCTTATAGTCAATGT 1979
Qy 2022 TTCTTTTATACATATTTATTAGTAAAGAAACATCATCTGAAATGTCTAGCTGCAAGTACA 2081
Db 1980 TTCTTTTATACATATTTATTAGTAAAGAAACATCATCTGAAATGTCTAGCTGCAAGTACA 2039
Qy 2082 TTCCTTTTGATGTGATATGGAAGAGTTAAAAAGGTGGAGAAATTCCTTGATTTCAACATGA 2141
Db 2040 TTCCTTTTGATGTGATATGGAAGAGTTAAAAAGGTGGAGAAATTCCTTGATTTCAACATGA 2099
Qy 2142 AATGCTCTCCTTTCCTCCCTGCSCCAAGAACCTTTTATGCCATTACCTPAGATTCACATATTC 2201
Db 2100 AATGCTCTCCTTTCCTCCCTGCSCCAAGAACCTTTTATGCCATTACCTPAGATTCACATATTC 2159
Qy 2202 TTTTAAATTTTCATCTCAGGCCCTCCCTCAACCCAC 2235
Db 2160 TTTTAAATTTTCATCTCAGGCCCTCCCTCAACCCAC 2193

RESULT      5
US-08-461-592B-1
: Sequence 1, Application US/08461592B
: Patent No. 5834425
: GENERAL INFORMATION:
: APPLICANT: Tedder, Thomas F.
: APPLICANT: Kansas, Geoffrey S.
: TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
: NUMBER OF SPOUNCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
: STREET: Ten Post Office Square
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/461,592B
: FILING DATE:
: CLASSIFICATION: 514

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PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/340,539
 FILING DATE: 16-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/008,459
 FILING DATE: 25-JAN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr.,
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: CG-104
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000
 TELEFAX: (212) 596-9090
 TELEX: 14-8367
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2330 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 53..1210
 OS-08-461-592B-1

Query Match	92.48;	Score 2087.6;	DB 2;	Length 2330;
Best Local Similarity	98.58;	Pred. No. 0;		
Matches 2161; Conservative	0;	Mismatches 24;	Indels 9;	Gaps 5

QY	44	CCCTTTGGCAAGGACCTGAGACCCCTTGCGTAAGTCAAGAGCCCTCATATGGCTCCACAAAG	1.03
Db	7	CCCTTTGGCAAGGACCTGAGACCCCTTGCGTAAGTCAAGAGCCCTCATATGGCTCCACAAAG	66
QY	104	AACTAGAGAAAGGACCAAGCAAAAGCCATGATATTTCCATGTGAAATGTCAAGACACCAGAG	1.63
Db	67	AACTAGAGAAAGGACCAAGCAAAAGCCATGATATTTCCATGTGAAATGTCAAGACACCAGAG	1.28
QY	164	GGACCTTATGSAACATCTTTCAGATTGTGGGGGTGACAAATGCTCTGTTGTGANTTCTGGC	2.23
Db	127	GGACCTTATGSAACATCTTTCAGATTGTGGGGGTGACAAATGCTCTGTTGTGANTTCTGGC	1.86
QY	224	ACATCATGGAACCTTACGTGCTGGAGATTACCATATTTCTCGAAAAACCCCTGTAACCTGGCAAAG	2.53
Db	187	ACATCATGGAACCTTACGTGCTGGAGATTACCATATTTCTCGAAAAACCCCTGTAACCTGGCAAAG	2.46
QY	284	GGCTAGAAAGATTCTGCCGAGACATTTACACAGATTTAGTTGGCTACACAAACCAAGGGGA	3.43
Db	247	GGCTAGAAAGATTCTGCCGAGACATTTACACAGATTTAGTTGGCTACACAAACCAAGGGGA	3.06
QY	344	AATTGAGTATCTGGAGAAAGACTTGCCCTTCAGTCCGTTCTTACTACTGATAGGAATCCG	4.03
Db	307	AATTGAGTATCTGGAGAAAGACTTGCCCTTCAGTCCGTTCTTACTACTGATAGGAATCCG	3.66
QY	404	GAAATATAGGAGGAAATATGAGAGTGGGTGGGGAACCAACAAATCTCTCACTAACAAGCAGA	4.53
Db	367	GAAATATAGGAGGAAATATGAGAGTGGGTGGGGAACCAACAAATCTCTCACTAACAAGCAGA	4.26
QY	464	GAACTGGGAGATGGTGAAGCCCAACACAAAGAAACAAAGAGAGACTGCGTGGAGATCTA	5.23
Db	427	GAACTGGGAGATGGTGAAGCCCAACACAAAGAAACAAAGAGAGACTGCGTGGAGATCTA	4.86
QY	524	TATCAAGAGAAACAAAGATGCAAGGCAAAATGGAACGATGACGCTGCCACAAACTAAAGGC	5.83
Db	487	TATCAAGAGAAACAAAGATGCAAGGCAAAATGGAACGATGACGCTGCCACAAACTAAAGGC	5.46
QY	584	AGCCCTCTGTACACACACTCTTTCGCCAGCCCTGTGTCAATGCAATGGCCATGTGACAAATGTCT	6.43
Db	547	AGCCCTCTGTACACACACTCTTTCGCCAGCCCTGTGTCAATGCAATGGCCATGTGACAAATGTGT	6.06

NAME: Gunnison, Jane
REGISTRATION NUMBER: 38,479
REFERENCE/DOCKET NUMBER: CG-104 CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1696 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-340-539A-11

Query Match 40.8%; Score 922.2; DB 1; Length 1696;
Best Local Similarity 97.8%; Pred. No. 3.9e-261;
Matches 989; Conservative 0; Mismatches 13; Indels 9; Gaps 5;

QY 1227 AGTATGATGACCCATTTAAATCGCCCTGGTGAAGAAATTCCTGGATACTAAAAA 1286
DB 308 AGTATGATGACCCATTTAAATCGCCCTGGTGAAGAAATTCCTGGATACTAAAAA 367
QY 1287 TCATGATGATCCTTTAAATCGCCCTGGTGAAGAAATTCCTGGATACTAAAAA 1346
DB 368 TCATGATGATCCTTTAAATCGCCCTGGTGAAGAAATTCCTGGATACTAAAAA 427
QY 1347 ACATGATGATG-TCCTTCATGATGATGGAAGATTTACCGGACCAAGTTCCTT 1405
DB 428 ACATGATGATGTCCTTCATGATGATGGAAGATTTACCGGACCAAGTTCCTT 487
QY 1406 CAGCTTCATTTGCGCCCTCATTTATCCCTCAACCCCGACGAGTGTATACAGC 1465
DB 488 CAGCTTCATTTGCGCCCTCATTTATCCCTCAACCCCGACGAGTGTATACAGC 547
QY 1466 TCAGCTTTTTCCTTTTCGAGGAGAAACAATAGAACCAT-AAGCGAAAGATTCATGT 1524
DB 548 TCAGCTTTTTCCTTTTCGAGGAGAAACAATAGAACCAT-AAGCGAAAGATTCATGT 607
QY 1525 GGAATATAGATGAGTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1584
DB 608 GGAATATAGATGAGTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 667
QY 1585 GCTGATGATGATGACAGACATTTCTAAATGAGTCAATTTGATACATATGTAATATG 1644
DB 668 GCTGATGATGATGACAGACATTTCTAAATGAGTCAATTTGATACATATGTAATATG 727
QY 1645 GACTCAGTTTCTGACAGATCAATTTCAAGTCTTCTTCTTCTTCTTCTTCTTCTTCT 1704
DB 728 GACTCAGTTTCTGACAGATCAATTTCAAGTCTTCTTCTTCTTCTTCTTCTTCTTCT 786
QY 1705 CTATTAAGAAAGTCAAAAGTCTAGTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCT 1764
DB 787 CT-----ATGAAGTCAAAAGTCTAGTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCT 841
QY 1765 GGTCTGCTCAAGTTGAAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1824
DB 842 GGTCTGCTCAAGTTGAAGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 901
QY 1825 CCATCTATTAACTGGCTTCAGGCTCCGACCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1884
DB 902 CCATCTATTAACTGGCTTCAGGCTCCGACCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 960
QY 1885 TGCTGATCTCCACAGCTACATCTATGATGTCAGCAAGCAAAAGAGAGAGAGAAAT 1944
DB 961 TGCTGATCTCCACAGCTACATCTATGATGTCAGCAAGCAAAAGAGAGAGAGAAAT 1020
QY 1945 AGCTGAGGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2004
DB 1021 AGCTGAGGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1080
QY 2005 TTCTTATAGTCAATGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2064

DB 1081 TTCTTATAGTCAATGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1140
QY 2065 GCTAGCTCAAGTACATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1214
DB 1141 GCTAGCTCAAGTACATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1200
QY 2125 TCCTTATGATGATGAAATGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2184
DB 1201 TCCTTATGATGATGAAATGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1260
QY 2185 CTAGATCTACATATATCTTAAATTTTCATGTCAGGCTCCCTCAACCCGAC 2235
DB 1261 CTAGATCTACATATATCTTAAATTTTCATGTCAGGCTCCCTCAACCCGAC 1311

RESULT 8
US-08-461-592B-11
Sequence 11, Application US/08461592B
Patent No. 5834425
GENERAL INFORMATION:
APPLICANT: Fedder, Thomas F.
APPLICANT: Kansas, Geoffrey S.
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurglin, Gagnebin & Hayes
STREET: Ten Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,592B
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/340,539
FILING DATE: 16-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: CG-104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1696 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-461-592B-11

Query Match 40.8%; Score 922.2; DB 2; Length 1696;
Best Local Similarity 97.8%; Pred. No. 3.9e-261;
Matches 989; Conservative 0; Mismatches 13; Indels 9; Gaps 5;

QY 1227 AGTATGATGACCCATTTAAATCGCCCTGGTGAAGAAATTCCTGGATACTAAAAA 1286


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||||| 369 GATAGGATAGGAAATTTGGAAATGTGGACATGGTGGGAAACCAAAATCTCTCAC 428
OY 452 TGAAGAAGAGAGAACTGGGGAGATGGTGAGCCCAACAAGAAAGAGAGACTG 511
Db 429 TAAAGAAGAGAGAACTGGGGTCTGGGGAGGCCAACAAAGAAATCCAAAGAGACTG 488
OY 512 CGTGGAGATCTATATCAAGAAACAAGATGCAAGGCAATGAGAGAGCTGGCA 571
Db 489 TGTGGATCTATATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 548
OY 572 CAAGCTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 631
Db 549 CAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 608
OY 632 TGGAGAGATGTAGAATATCATATATCAACAGCTGCAAGCTGAGTGGGTACTATG 691
Db 609 TGGAGAGATGTAGAATATCATATATCAACAGCTGCAAGCTGAGTGGGTACTATG 668
OY 692 GCGCCAGTGTAGCTGTGTATTCAGTGTAGAGCTTTGGAGGCCCAAGAGAGCTGGTACAT 751
Db 669 GCGCCAGTGTAGTATGTGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 728
OY 752 GGCATGTACTACCCCTTGGAAACTGAGCTTCAAGCTGAGCTGAGCTGAGCTGCTC 811
Db 729 GGCATGTACTACCCCTTGGAAACTGAGCTTCAAGCTGAGCTGAGCTGAGCTGCTC 788
OY 812 TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 871
Db 789 TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 848
OY 872 ATCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 931
Db 849 ATCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 908
OY 932 GATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 991
Db 909 TACCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 968
OY 992 CTGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1051
Db 969 CTGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1028
OY 1052 CTGGCAAACTCTGATATGCAAAATTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1111
Db 1029 CTGGCAAACTCTGATATGCAAAATTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1088
OY 1112 GGGGATATTAACCCCTCTTCATTCAGTGGAGTCAATGTTACTGATCTCTGGGCT 1171
Db 1089 AGGTGACTACAACCCCTCTTCATTCAGTGGAGTCAATGTTACTGATCTCTGGGCT 1148
OY 1172 GGCATTTATCTTTGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1231
Db 1149 GGCATTTATCTTTGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1208
OY 1232 GAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1284
Db 1209 GGCATGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1268
OY 1285 AATCATGAGATCTCTTAAATCTTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1344
Db 1269 CATTCGAAATTAAGCTGAGTCCCGTGAAGATTTTAAACGAGAGAGAGAGAGAGAT 1328
OY 1345 AATCATGAGATCTCTTAAATCTTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1404
Db 1329 AGGATGAGATCTCTTAAATCTTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1386
OY 1405 TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1464
Db 1387 CTTAATTTCCCTTCGCTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1446
OY 1465 CTGAGCTTTTGTCTTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1524
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Db 1447 AGTAGATTTATCATCTTTTCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1497
OY 1525 GGAATATAAGATGAGTCTGATCTTTGCTTTTGTGAGCTTTTGTGAGTTCATTCAT 1584
Db 1498 AGAATATAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1557
OY 1585 GCTGACTTGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1644
Db 1558 ACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1607
OY 1645 GACTGAGTCTTGTGAGAGAT 1664
Db 1608 AACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1627
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RESULT 10
5514582-3
; Patent No. 5514582
; APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A.
; TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
; IMMUNOLOGICALS
; NUMBER OF SEQUENCES: 43
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,670
; FILING DATE: 21-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 986,931
; FILING DATE: 08-DEC-1992
; APPLICATION NUMBER: 808,122
; FILING DATE: 16-DEC-1991
; APPLICATION NUMBER: 440,625
; FILING DATE: 22-NOV-1989
; APPLICATION NUMBER: 315,015
; FILING DATE: 23-FEB-1989
; SEQ ID NO:3
; LENGTH: 2214
5514582-3
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Query Match 37.9%; Score 856.8; DB 5; Length 2214;
Best Local Similarity 73.4%; Pred. No. 7.3e-242;
Matches 1160; Conservative 0; Mismatches 392; Indels 28; Gaps 4;

OY 92 GGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 151
Db 69 ggcctgagagagagagagagagagagagagagagagagagagagagagagagagag 128
OY 152 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 211
Db 129 gggtaacttacttgggagagagagagagagagagagagagagagagagagagagag 188
OY 212 TGAATTTCTTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 271
Db 189 tgacttctcgtatcacacagagagagagagagagagagagagagagagagagagagag 248
OY 272 GAACTGGCAAAAGGCTGAGAGATTCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 331
Db 249 gaactgggaatagctagagagagagagagagagagagagagagagagagagagagag 308
OY 332 AATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 391
Db 309 aaacaagagagagagagagagagagagagagagagagagagagagagagagagagag 368
OY 392 GATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 451
Db 369 gatagaagatcaggaagagagagagagagagagagagagagagagagagagagagag 428
OY 452 TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 511
Db 429 taagaagagagagagagagagagagagagagagagagagagagagagagagagagag 488
OY 512 CGTGGAGATCTTATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 571
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Dh	489	tgtagagatcctatatacgaagaggaagagactctcggaaatatgaaagatgaaagcctcgta	548
Qy	572	CAAACTAAAGGCAGCCCTCTGTACAGACGCTCTTGGCCAGCCCTGTGATGACATGGCCA	631
Dh	549	caaaagaaagcagcgtctctctctacaaagcctctctgcagccagcgtctctgcaatgycg	608
Qy	632	TTGGAGATATGTGTAGAAATCATCATTAATCACACCTGCGAACTGTGATGTGGGGTACTATGG	691
Dh	609	tggagaaatgctgtagaaactatacaacaatacaacgtgcatactgtatgtacaggtataatcag	668
Qy	692	GGCCCCAGTGCAGCGCTTGATATTTTCAGTGTGAGACCCCTTTTGAGGCCCCGACAGCTGGGTACCAAT	751
Dh	669	gcccaagtcgtaataatgtagtgcagtgcaagtgcaagcctctggaagccccgagatctggtatacat	728
Qy	752	GGACGTGTACTCAGCCCTTTTGGAAACCTTCAGCGCTTCAGCTCAGAGTGTGCTCTTCAGCTGCCTC	811
Dh	729	ggaactgaaatccacccctctgggaactctcagctctccagttccaaatgtgctctcaactcgctc	788
Qy	812	TTGAGGAACAAACTTAACTGGGATTTGAAGAAACCCTGTGGACCAATTTGGAACTGGTC	871
Dh	789	tggaggaagagagactactctggaactgcagaaaacaagtgtagagcactctggaactcgttc	848
Qy	872	ATCTCCACAACCAACCGTGCAGAGTGATTTTCAGTGTGAGCCCTTAACTCAGACCAATTTGGG	931
Dh	849	atctccaaagccaaactcgcgaagtcgcagtgtagcctctggaagccccgagatcttgg	908
Qy	932	GATCATGAACTGTAGCCATCCCGCGGCGAGCTTCAGCTTCACCTGTGATGTACCTTCAT	991
Dh	909	tacaatgtagcgtgcatctccaccctctgggaataacttcagctccaaatgtagtcttcaa	968
Qy	992	CTGCTCAGACGAACTGAGTTAATTGGGAAAGAAACAATTTGTGTAATCTGTGAAT	105
Dh	969	ctgtctctgaggaagagagagactctggaactcgcagaacaacagtgtagcactctgaa	1022
Qy	1052	CTGGCTAAATCTGTGCCAATATGTCAAAAATTGGACAAAAGTTTCATGATTTAAAGA	111
Dh	1029	ctggacatctccagagaaacatcgcgaagaaacaagaagatctctcaagaataccaaga	108
Qy	1112	GGGTGATTAATAACCCCGCTTCATTTCCAGTGGCAGTATGTTACTTGATCTCTGGATT	117
Dh	1089	agtgtagcaacaacccccctctcatctctctgtacgcgtcaigtctcaacgcctctccggct	114
Qy	1172	GGCATTTATCATTTTGGCTGCGAGAGAGATTTAAAAAAGCGAAGAAATCCAGAAGATAT	123
Dh	1149	ggcaattctcatcttgcgtcgcgaagcggcttaaaaaagcaagaatctcaagaagaagat	120
Qy	1232	GAATGACCCATATTAAATATGCCCGCTGGTGMAAAGAAATTTCTTG-----GAATACTAA	128
Dh	1209	ggaatgataccatacgaatcatcctcttggaaaggaagccaatgaagtgctaaagaataa	126
Qy	1285	AATCATGTGATCTCTTTAAATCTTTCATGAAACGTTTGTGTGGGACACTCTCACTGC	134
Dh	1269	catggaataataaaggtcaagtcacctcccggtgaagaattttaaagcgagcatctccacat	132
Qy	1345	AAACATGAATGTGTGTCTCTTCAGTGATCTGTGGAGATTTTCTACCGGACCAACGTTCT	140
Dh	1329	agagtagcagtgcttgc-----tcaacgaatctgcgaagatcttctcatcgcacaacagctct	138
Qy	1405	TCACGTTCCATTTTGGCCCGTCATTTATTCCTCAACCCCGACGCCACAGGTGTTATACAG	146
Dh	1387	ctcaattctccctctgcatcatcaccataccaacttaccataaagtgtagtctatacag	144
Qy	1465	CTCAGCTTTTGTCTTTTCTTGAGAGAAACAAATAAGACCAATGAAGGAAAGATTCATGT	152
Dh	1447	agtgtatattatcatcctctctcgtgtaggaac-----aagcaaaagtgctacgct	149
Qy	1525	GGAAATATTAAGATGGCTGACTTTTGCTTTTCTTGACTCTGTGTTTTCAGTTTCAATTAAT	158
Dh	1498	agaataataaagaacgctgcttctacctcttcccaactcgtcttctcctagtgtaaatccag	155
Qy	1585	GCTGTACTTTCATGCACAGACACTTTAAATGAATGCAAAATTTGCATATGTGGAATATG	164
Dh	1558	acaaagagctaaatgcacaaac-----agtgaaataatgatacatcagatgaattcga	160

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QY 1645 GACTCAGTTTCTTGCAAGT 1664
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Db 1608 aactcagactccttgccgat 1627

RESULT 11
US-08-340-539A-5
; Sequence 5, Application US/08340539A
; Patent No. 5808025
; GENERAL INFORMATION:
; APPLICANT : Tedder, Thomas F.
; APPLICANT : Kansas, Geoffrey S.
; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
; TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,539A
; FILING DATE: 16-NOV-1994
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,459
; FILING DATE: 25-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gunnison, Jane
; REFERENCE/DOCKET NUMBER: 38, 479
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9090
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 531 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-340-539A-5

Query Match 17.1%; Score 385.2; DB 1; Length 531;
Best Local Similarity 99.2%; Pred. No. 1.2e-103;
Matches 387; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 213 GATTTCCTGCGACATCATGTGGAACCTCACTGCTGAGCTTACCATTTATTTCTGAAAAACCCATG 272
Db 72 GATTTCCTGCGACATCATGTGGAACCGACTGCTGACTTACCATTTATTTCTGAAAAACCCATG 131

QY 273 AACTGCGAAGGGCTAGAGAATTCTGCCGAGACAATTACACAGATTAGTGGCATTCACA 332
Db 132 AACTGCGAAGGGCTAGAGAATTCTGCCGAGACAATTACACAGATTATTTAGTGGCATTCACA 191

QY 333 AACCAAGGCGGAATTGAGTATCTGGAGAGAAGACTTGCCTTCAGTTCGTTCTTACTACTG 392
Db 192 AACCAAGGCGGAATTGAGTATCTGGAGAGAAGACTTGCCTTCAGTTCGTTCTTACTACTG 251

QY 393 ATACGAATTCGGGAAGATAGAGAGATATGAGACTGGGTGGGAGAACCAACAAATCTCTCACT 452
Db 252 ATATGGAATTCGGGAAGATAGAGAGATATGGAAGTGGGTGGGAGAACCAACAAATCTCTCACT 311

QY 453 GAAGAAGCGAAGAACTGGGGAGATGGTGAAGCCCAACACAGAAACAGAGAGACTGG 512

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Db      899 ctcccatggaacaacacgtacattgactgtgtaagaagattgactaatggagc 958
Qy      1022 GAAGAAACCATTTGTGAATCATCTGTAATCTGTAATCTCTGTAATATGTCAA 1079
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db      959 ccagaagcctcagtgtaacctcctggaattggacacacgaagaacgaacgtgtaaa 1016

RESULT 15
US-08-365-470-1
; Sequence 1, Application US/08365470
; Patent No. 5632991
; GENERAL INFORMATION:
; APPLICANT: Gimdione, Jr., Michael A.
; TITLE OF INVENTION: Antibodies Specific For E-selectin And The Uses
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/365,470
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,510
; FILING DATE: 05-AUG-1993
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/850,802
; FILING DATE: 13-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Markowicz, Karen R.
; REGISTRATION NUMBER: 36,351
; REFERENCE/DOCKET NUMBER: 0627.1350003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3854 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-365-470-1

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Query Match      13.7%; Score 310; DB 1; Length 3854;
Best Local Similarity 60.6%; Pred. No. 4.1e-81;
Matches 508; Conservative 0; Mismatches 330; Indels 0; Gaps 0;

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Qy      482 GCCCAACAAGAAAGAACAGAGAGACTGCGTGAGATCTATATCAAGAAACAAGA 541
      111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
Db      419 ACCCAACAATTAAGGCAAAAAAGATGAGAGACTGCTGAGATCTTACATCAAGAAAGAAAAGA 478
Qy      542 TGCAGGCAATATGGAACGATGAGCGCTGACCAAACTAAAGCGAGCCCTGTTACACAGC 601
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Search completed: January 12, 2001, 21:40:23
 Job time: 18969 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2001, 20:32:12 : Search time 2169.06 Seconds
(Without alignments)
3694.857 Million cell updates/sec

Title: US-09-119-209-1

Perfect score: 2259
Sequence: 1 GAATTCACACTGCTGGCTT.....CCGCACGACACTGGAATTC 2259

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 12197726 seqs, 1773875003 residues

Total number of hits satisfying chosen parameters: 24395452

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2259	100.0	2259	15 US-09-119-209-1	Sequence 1, App1
2	2161	95.7	2354	14 US-09-023-655-1154	Sequence 1154, Ap
3	2151.6	95.2	2385	49 US-60-243-521-8	Sequence 8, App1
4	2150	95.2	2385	46 US-60-213-360-1118	Sequence 1118, Ap
5	2150	95.2	2385	46 US-09-396-970-8450	Sequence 8480, Ap
6	2146.8	95.0	2385	36 US-60-118-318-292	Sequence 292, App
7	2129.6	94.3	2387	42 US-60-172-373-15742	Sequence 15742, A
8	2087.6	92.4	2330	1 PCT-US92-03970-1	Sequence 1, App1
9	2087.6	92.4	2330	1 PCT-US94-00909-1	Sequence 1, App1
10	2087.6	92.4	2330	4 US-08-008-459-1	Sequence 1, App1
11	2087.6	92.4	2330	7 US-08-340-539-1	Sequence 1, App1
12	2087.6	92.4	2330	8 US-08-410-569-1	Sequence 1, App1
13	1605.4	71.1	1788	41 US-60-164-285-5439	Sequence 5139, Ap
14	1605.4	71.1	1788	41 US-60-164-285-5439	Sequence 5139, Ap
15	1006.4	44.6	3238	46 US-60-212-659-230	Sequence 816, App
16	959.2	42.5	3238	46 US-60-212-659-230	Sequence 230, App
17	959.2	42.5	3238	46 US-60-212-659-230	Sequence 754, App
18	948.2	42.0	3233	45 US-60-207-315-164	Sequence 164, App
19	922.2	40.8	1696	1 PCT-US92-03970-1	Sequence 11, App1
20	922.2	40.8	1696	1 PCT-US94-00909-1	Sequence 11, App1
21	922.2	40.8	1696	4 US-08-008-459-1	Sequence 11, App1
22	922.2	40.8	1696	7 US-08-340-539-1	Sequence 11, App1
23	922.2	40.8	1696	8 US-08-410-569-1	Sequence 11, App1
24	856.8	37.9	2214	15 US-09-119-209-3	Sequence 3, App1
25	682.6	30.2	3238	48 US-60-230-435-2748	Sequence 2748, Ap
26	556.6	24.6	745	17 US-09-396-970-8450	Sequence 5762, Ap
27	475.4	21.0	519	17 US-09-396-970-8450	Sequence 6256, Ap
28	451.2	20.0	505	55 US-09-726-811-2121	Sequence 2121, Ap
29	428.2	19.0	487	17 US-09-359-067-46139	Sequence 46139, A
30	420	18.6	434	19 US-09-528-409-11317	Sequence 11317, A
31	407.6	18.0	421	19 US-09-528-409-11317	Sequence 11317, A
32	405.6	18.0	528	16 US-09-240-371-9103	Sequence 9103, Ap
33	402	17.8	504	23 US-09-652-816-2022	Sequence 2022, Ap
34	401	17.8	435	17 US-09-399-720-6114	Sequence 6114, Ap
35	401	17.8	464	16 US-09-289-768-1303	Sequence 1303, Ap
36	394.4	17.5	492	55 US-09-726-811-1825	Sequence 1825, Ap
37	393.4	17.4	464	17 US-09-359-067-41757	Sequence 41757, A
38	386	17.1	454	55 US-09-726-811-1825	Sequence 1825, Ap
39	385.6	17.1	454	17 US-09-359-067-42217	Sequence 42217, A
40	385.6	17.1	454	19 US-09-528-409-117248	Sequence 107248, A
41	385.2	17.1	531	1 PCT-US92-03970-5	Sequence 107248, A
42	385.2	17.1	531	1 PCT-US94-00909-5	Sequence 5, App1
43	385.2	17.1	531	4 US-08-008-459-1	Sequence 5, App1
44	385.2	17.1	531	7 US-08-340-539-5	Sequence 5, App1
45	385.2	17.1	531	8 US-08-410-569-5	Sequence 5, App1

ALIGNMENTS

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RESULT 1
US-09-119-209-1
; Sequence 1, Application US/09119209
; GENERAL INFORMATION:
; APPLICANT: LASKY, LAURENCE A.
; APPLICANT: STACHELL, SCOTT E.
; APPLICANT: ROSEN, STEVEN D.
; APPLICANT: SINGER, MARK S.
; APPLICANT: YEDNOCK, TED A.
; TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/119, 209
; FILING DATE: 20-Jul-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/513278
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/059027
; FILING DATE: 6-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/786149
; FILING DATE: 31-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/315015
; FILING DATE: 23-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0565D1C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SBO ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2259 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
;
; US-09-119-209-1
;
Query Match 100.0%; Score 2259; DB 15; Length 2259;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1752 GGGGCTGCTGAG 1811
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RESULT 3
US-60-243-521-8
; Sequence 8, Application US/60243521
; GENERAL INFORMATION:
; APPLICANT: Hopkins, Christopher M.
; APPLICANT: Peterson, David P.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: GENES REGULATED IN ACTIVATED T CELLS
; FILE REFERENCE: PA-0042 P
; CURRENT APPLICATION NUMBER: US/60/243,521
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PERL Program
; SEQ ID NO 8
; LENGTH: 2385
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Template ID: 331616.2
US-60-243-521-8

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					Gaps 4;
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OY	84	GGCTCAATGGCGCTGCAGAGAAGTAGAGAGACCAACCAAGCCATATATTTCCATAG	143		
DB	92	ggctcaatggcgctgcagagaagactagagaagaccagcaagccaatgatatcttcag	151		
OY	144	AAATGTGAGACACCCAGAGGACTTATGACATCTTCAAGTTGGGGGTGACAAATG	203		
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DB	212	ctctgtgtgtatcttccttgccatcatatggaacccagctctggaacttaccatctctgaa	271		
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DB	392	tactacttgatagaaatccggaaagatlaagagaaataltgaaagctgggtgggaaccaaaa	451		
OY	444	TTCTGCACTGGAAGACGAGAACTGGGAGATGGTGAGCCCAACAAGAAAGAAACAG	503		
DB	452	ttcttctactggaagagacgagaaactcggggagatggttgagcccaaaaagaagaacaag	511		
OY	504	GAGAGACTGCTGAGATCTTATATCAAGAAACAAGATGAGGCAAAATGGAACGATGAC	563		
DB	512	gagagactcgttgagagatctatatcaagaaacaaagatgcaggaataatggaacgaatgac	571		
OY	564	GGCTGGCCAAACTTAAGGCAAGCCCTCTGTTTACACAGCTTCTTGCCAGCCCTGGTCAATGC	623		
DB	572	ggctggccaaaactlaaagcagccctctgttacaacagctcttgcagccctggtcaltgc	631		
OY	624	AGTGGCCATGAGAAATGTGTAATAATCATATATACACTGTGCACTGTGATGTGGGG	683		
DB	632	agtggccatgagaaatctgttagaataatcaataatcaccttgcaacttgatggtgggg	691		
OY	684	TACTATGGGCCCCAGTGTCACTTGTGATTCAGTGTGAGCTTTGAGAGGCCCCAGAGCTG	743		
DB	692	tactatgggcccagctgtcagatctgtgtatcagtgtagagccttgggaagcccacgaagctg	751		
OY	744	GGTACCATGGAAGCTGACTTACCCCTTTGGAAACTTTCAGCTTTCAGCTTCACAGTGTGCCCTTC	803		
DB	752	gttaccaatggaactgttacccaccttggaaacttcagcttcagcttcacagtggtcccttc	811		
OY	804	AGCTGCTCTGAAGAGAACAACTTAACGTGGGATTTGAAGAAACACCCTGTGGACCAATTTGGA	863		
DB	812	agctgctcttgaagaaacaaacttaactctggatctgaagaaacacactgtggaccatcttga	871		
OY	864	AACTGTCATCTCCAGAACCAACTGTCAAGTGAATTCAGTGTGAGCCCTTTCAGACACCA	923		
DB	872	aaactgctcatctccaagaacaaactgtcaagtgatctcagtggtggtccctctacagacaca	931		
OY	924	GATTTTGGGATCATGAACGTGATGACCAATCCCTGGCCAGCTTTCAGCTTTTACCTCTTGCAATG	983		
DB	932	gatltgggatactgaacactgtagccatcccttggccagcttcacagcttlaacctctgcaatg	991		
OY	984	ACCTTCATCTCTCGAAGAGAACTGAGTTAATTTGGAGAGAGAAACCAATTTTGCATATCA	1043		
DB	992	accttcatctctcagaagaaactgaglttaaatctgggaagaaacaaacatcttgaaatca	1051		
OY	1044	TCTGGAATCTGTGTAATCTAGTCAATATGTCAAAAATTTGACAAAAGTTTCTCATATG	1103		

DB	1052	ctcggaaactcgtgccaaatccatccatagtcacaaatctgacaaaagcttccaaatg	1111
OY	1104	ATTAAGGAGGGGTGATTAATAACCCCTTTCATTTCCAGTGGCAGTCAATGTTACTGCATTC	1163
DB	1112	atlaaggaagggtgattataaaccctcttcatctcagtggaagtcatactgtaactgcatc	1171
OY	1164	TCTGGGTTGGCATTTATATTTTGGCTGGCAAGGAATTTAAAAAAGCAAGAAATTCAG	1223
DB	1172	ctcgggttggaacttatcatctatctgtgcgaaggaatcaaaaaagagcaagaatccaaag	1231
OY	1224	AGAACTATGAATGACCCATATTTAATCGCCCTTGGTGAAGAAATTTCTTGGAAATATCA	1283
DB	1232	agaagtatgaatgaaacccatatlaaatcgcccttgggtgaagaanaatctctgaaatcaaa	1291
OY	1284	AAATCATGAGATCCCTTTAAATCCCTTCATGAAACGTTTGTGTGCTGGCACCCTCTACGT	1343
DB	1292	aaatcatgagatcccttlaaatcccttccatgaaacgtcttggtggcacccctcactagct	1351
OY	1344	CAAACTGAAGGTG-TTCCCTTCAGTGCATCGGGAAGATTTCTACCCGACCAACAGTTTC	1402
DB	1352	caaaactgaagtggtcttcccttcagtgcatctgggaagatctctaccgacaacagatctc	1411
OY	1403	CTTGACCTTCATTTCCGCCCTCATTTATCCCTCAACGCCACGACCACAGTGTATTATAC	1462
DB	1412	cttcagcttccatctgcgccctcatcttaaccccaaccccaagcccaagtgcttatagc	1471
OY	1463	AGCTAGCTTTTGTGCTTTTCTTGAGAGAGAACAAATTAAGACCAT-AAGCGAAAGCAATTC	1521
DB	1472	agctagcttcttctctcttcggaagaaacaaatlaagaaacatlaaaggaagaaatctca	1531
OY	1522	TGTGGAATATAAGATGGCTGACTTGTGCTTCTTGACTCTTGTTTCACTTGCATATTC	1581
DB	1532	tgtggaatataaagatgagctgactcttgccttctcctgcagctctgtcttcaagttcaatcc	1591
OY	1582	AGTGTACTTGTGATGACAGACACTTCTAAATGAAGTGCAAATTTGATATCATATGTGAT	1641
DB	1592	agtgctgacttgatgagacagacactctaaatgaagtgcaaatctgatacatatgctgaa	1651
OY	1642	ATGGACTAGTTTTTCTTGACAGATCAAAATTTTACAGCTGCTTCTGTATCTGTGACGATAC	1701
DB	1652	atggactagtttcttctgcaabatacaaatcttcaagctgcttctgtatctgtgagagctac	1711
OY	1702	ACTCTTATGAAGATTCAAAAGTCTACGCTCTCTTCTTCTTCAATCCGATGGAATTA	1761
DB	1712	actcttataagaagatccaaaagctcagctcctcttcttcttcaaccccaagtgaaatca	1771
OY	1762	TGGGGTCTGTGCAAGTGAAGAGATCCCTATTTGCACGTGATGACCTCGGCGTGTGGAAT	1821
DB	1772	tggggtctgtcagatctgaaagagctctatcttgcaactgtagccctgcgcctctgaaatc	1831
OY	1822	GGACCATCTCTAATTAAGTGGCTTCAGGCCCTCCACCTTTCAGCCACCTCTCTTTTTC	1881
DB	1832	ggaccatctctatlaaacggtctca-gcctcccaaccttctcagcccaacctctcttcttc	1890
OY	1882	AGTGGCGTACTTCCACACCTCAAGCTCATGTCATGAGTGGCCAAAGAAAGAGAAAGAGA	1941
DB	1891	agtggcgacttccacaccagatctcactcagtgagtgcaagcaaaagtagaagaagaga	1950
OY	1942	AATAGCCTGCGCGGTTTTTATGTTTGGGGGTTTTGCTTTTCCTTTTATGAGACCAATTC	2001
DB	1951	aatagccgcgctgtcttcttgatcttggtgggtcttgctgtcttccctctatgaaacccatc	2010
OY	2002	CTAATTTCTTAATGTCATATGTTTCTTTTATACAGATATTTAATTAAGAAACATCATCTGA	2061
DB	2011	ctaatcttctatagtcataagcttcttcttcaagatcatatctagtaagaacacatacctga	2070
OY	2062	AATGCTAGCTGCAAGTGCATCTCTTGTGATGTCATATGGAAGAGATTAAACAGGTGGAGA	2121
DB	2071	aatgctagctgcaagtgcaatcctcttgatgcatatggaagagcttlaaacaagtggaaga	2130
OY	2122	AATTCCTTGATTCACAAAGAAATGCTCTCTTCCCTCGCCCCGAGAACTTTTATCAGCT	2181

Db 2131 aatcccttgatccaacatgaaatgctctccctccctccgccccagacttataccact 2190
QY 2182 TACCTAGATTCACATATTTCTTAATTTTCATCTCAGGCCCTCCCTCAACCCAC 2235
Db 2191 tacttagattacatatcttcttaattcaatcccaaggcccccacacccac 2244

RESULT 4
US-60-213-360-1118
; Sequence 1118, Application US/60213360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Ial, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; FILE REFERENCE: GX-0014 P
; CURRENT APPLICATION NUMBER: US/60/213,360
; NUMBER OF SEQ ID NOS: 8347
; SOFTWARE: PERL Program
; SEQ ID NO 1118
; LENGTH: 2385
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID NO: 331616.2
US-60-213-360-1118

Query Match 95.2%; Score 2150; DB 46; Length 2385;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2200; Conservative 0; Mismatches 10; Indels 4; Gaps 4;

QY 25 ACCTGACGACAGCACATCCCTTT-GGCAAGGACCTGAGACCCCTGTCATAGTCAGA 83
Db 32 accctgagcaacagcaactccctcttggcaagaccctgagacccttgcctaaagca 91
QY 84 GCCTCAATGGCTGCGAGAGAACTAGAGAGAGGACCAAGCCAGATGATTTCCATGG 143
Db 92 ggtcaaatggctgcaagaagactagagaagaccagaagccatgatatctccatg 151
QY 144 AATGTCAGACACCCCAAGGACTTATGGAACATCTTCAAGTTGTGGGGTGGACATG 203
Db 152 aaatgctagacacccagaggaactatcgaaactctcaagtgtggtggtgacaatg 211
QY 204 CTCTGTTGATTTCTGCGACATCATGGAACCTACTGCTGACTTACCATTTATTTGAA 263
Db 212 ctctgtgtgtcttctcctgacatcatggaaccgactgctgacttaccattctcgaa 271
QY 264 AAACCCATGAACCTGGCAAGGCGCTAGAGATTTCTGCCGAGACAAATTACAGATTTAGTT 323
Db 272 aaacccatgaacttggcaaaaggctagaagaattctgccgaacaattacacaagattagtt 331
QY 324 GCCATACAAAAGGCGGAATTTGATCTCTGAGAGACTGTGGCCCTTCACTGCTCT 383
Db 332 gccatacaaaagaaggggaattgtatctctgagagaagctctgcttccagtcgtct 391
QY 384 TACTACTGATAGGAATCCGGAAGATAGAGAAATGACGCTGGGTGGAAACCAAAA 443
Db 392 tactacttggatagaaatccggaagatagagaaatatgacgtggtggaaccaaaaa 451
QY 444 TCTCTCACTAAGAGAGAGACTGGGAGATGGTGGACCCCAACAAGAAAGAAAGCAAG 503
Db 452 tctcttaacttgaagaagacgtggtggtggtggtggtggtggtggtggtggtggtggt 511
QY 504 GAGGACTGCTGGAGATCTATATCAAGAGAAACAAGATGACGCAAAATGGAACGTGAC 563
Db 512 gaggaactgcttgaagatctatacaagagaacaaagatgacgagcaaatggaacgtgac 571
QY 564 GCCTGCACAAACTAAAGGACCCCTCTGTACACAGCTTTCTTGGCCAGCCCTGATCATG 623

Db 572 gccctcccaaaactaaagcaagccctctgttaccagaagcttcttgcagccctgtatgc 631
QY 624 AGTGGCATGAGAGATGTTGTAAGTAATCATATCAATATATCATCAGCTTCAACTGTATGGG 683
Db 632 agtggcatagagaagatgtgtgaagaatcacaataatcaacttcaacttgaatgtggtg 691
QY 684 TACTATGGGCCCACTGTGACCTTGTGATTCATGCTGTGAGCTTGGAGGCCCAAGACTG 743
Db 692 tactatggccccagtgctcagttgtgtatctatgagtgtgagcccttggagcccaagactg 751
QY 744 GGTACATGAGACTGACTACCCCTTTGGAAACTTCAGCTTCAGCTTCAGCTGAGCTTC 803
Db 752 ggtacacatggaacttactcaacccttgggaacttcaacttgcagcttccagctcagtgcttc 811
QY 804 AGCTGCTCTGAAGAACAAACTTAACTGAGGATTGGAACAAACCACTGTGACCATTTGGA 863
Db 812 agctgctctgaagaagaaacttaactgagatggaagaacacacccgtggaacatttga 871
QY 864 AACTGTGATCTCCAGAACCAACCTGTCAAGTGTCAAGTGTGAGGCTGTATCAGCACA 923
Db 872 aactgtcatctccagaacacacgttcaagtgattcagtggtgagctctatcagaccca 931
QY 924 GATTGGGATCATGAGACTGAGCATCCCTGGGCCAGCTTCAGCTTACCTGTGATGT 983
Db 932 gattgggatcatgaaactgtgagcatcccttggcagacttcaagcttacccttgcattgt 991
QY 984 ACCTTCATCTGCTCAGAGAGAACTGATTAATTTGGAGAACAAACATTTGTGATGATCA 1043
Db 992 acccttacccttgcacagaagaaactgtaatttgggaagaagaacacatctgtgaatca 1051
QY 1044 TCTGGAATCTGTCGAATCTTACTTCAATATGTCAAAAATTTGGACAAAAGTTTCTCAATG 1103
Db 1052 tctggaaacttggcaaatcccttgaatcacaatgtcacaataatgtgcaaaaagtcttccaatg 1111
QY 1104 ATTAAGGAGGCTGATTTAATTAACCCCTTCATTCACAGTGGCGATGTTACTACATTC 1163
Db 1112 attaaggaagggtattataaacccttccatctcagtgagcgtacatgacttgcattc 1171
QY 1164 TCTGGGTTGGCATTTATCATTTTGGCTGGCAGAGAGATTAATAAAGGACAGAAATCCAG 1223
Db 1172 tctgggttggcatcttcaatcttgccttgcaggaagatataaagaagaagaatccaa 1231
QY 1224 AGAAGTATGAATGACCCATTAATTAATCGCCCTTGGTGAAGAAATTTGTGATTAATA 1283
Db 1232 agaagatgaatgacccatataataatgccttcttggtaagaataatcttgyaatactaa 1291
QY 1284 AATCATGAGATCTTTAATCTTCATGAAACGTTTTGTGTGGTGGACCTCTACGT 1343
Db 1292 aatcatgagatcctttaaactccttccatgaaagcttctgtgtgtgacacctcctcgt 1351
QY 1344 CAACATGAGAGTGTG-TTCCTTCATGATGATCTGGAGAGATTTTCAACCCAGCAACAGTTC 1402
Db 1352 caaacatgaagtgttcttccctcagtgcatcttgggaagattcttcaacttgcacaaagctc 1411
QY 1403 CTTCAGCTTCATTTGCCCCCTCAATTTATCCCTCAACCCAGCCACAGGTGTTATAC 1462
Db 1412 ctctcagcttccatttgcgcccctcatcttaaccctcaaccccaagcccaagtgcttatac 1471
QY 1463 AGCTAGCTTTTGTCTTTTGTGAGAGAAACAATTAAGACAT-AAAGGAAGAGATTGA 1521
Db 1472 agctcagcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1531
QY 1522 TGTGAAATTAAGATGAGCTGATCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1581
Db 1532 tgtgaaataataaagatgctgacttcttcttcttcttcttcttcttcttcttcttcttct 1591
QY 1582 AGCTGCTACTTGTGACAGACACTTCTAATGAAGTGAATTTGATATGATATGGAAT 1641
Db 1592 agtctgtacttcttgaacagacacttcaataagaatgaaatcttgaatcatatgtgact 1651
QY 1642 ATGAGCTCAGTTTCTTGACGATCAATTTTCAAGCTGTCTCTGTATCTGTTGAGAGTAC 1701

Db	1652	atgagactcagttctctctgcgcagatccaattctcaagtcgctctctctgtatctatctgtgagagttac	1711
OY	1702	ACTCTTATAGAAAGTTCCAAAAGCTCTACGCTCTCTCTTTCTTATCTAATCTCCAGTGAAGTAA	1761
Db	1712	acctctatagaagttcaaaaaagcttaagctctctctctctctctctctcaactccagtgaaagta	1771
OY	1762	TGGGGTCTCGTCAAGTTTGAAAAGATCTATTTTGACACTGACCTGCGCGTCTGTGAATT	1821
Db	1772	tggggtctctgctcaagttcaagaagttcctaattgtcacgttgagctctgcgtctgtgaatt	1831
OY	1822	GCAGCATCTCTTTTAACTGGCTTCAGGCGCCGCCACCTTCCTTTCAGCACTCTCTTTTTC	1881
Db	1832	ggacacacctcttaacttggtcttca-gcctcccaacctctctctcaagccacctctctcttct	1890
OY	1882	AGTTGGCTGACTTTCACACCTTAGCATCTCATGATGCCAAGCAAAAGAGAGACAGAGA	1941
Db	1891	agttggctgactctccacacttagcatctcatctgagtgccaaagaagaagagagaagaga	1950
OY	1942	AATAGCTCGCGGTTTTTTAGTTTGGGGTTTTGCTGTTTCTTTTATGAGACCATTC	2001
Db	1951	aatagcctgcgctgtcttctttagttctgggggttctgctgtctctctctctctctctctctct	2010
OY	2002	CTATTCTTATAGTCATCTGTTCTCTTTATCAGCATATTAATAGTAAGAAAACATCATCTGA	2061
Db	2011	ctattctctatagaagctcagct	2070
OY	2062	AATGCTAGCTCAGTACATCTCTTTTGATGTGATATGGAAGAGTTTAAACAGTGGAGAGA	2121
Db	2071	aatgctagctgcgaagtgaactctctcttgatgcatactgaagaagttaaaacaggtggaga	2130
OY	2122	AATTCTTTGATTCAATGAAATGCTCTCTTTCCCTGCCCCAGAACTTTTATCCACT	2181
Db	2131	aattctcttgattcacaatgaagaatgctctctctctctctctctctctctctctctctctctct	2190
OY	2182	TACCTAGATTCTACATATCTCTTTTAAATTCATCTCAGCGCTCCGCAACCCAC	2235
Db	2191	tacctagattctcacatactctctcttaaatctctcaagctctctctctcaaccac	2244
RESULT 5			
US-09-396-970-8480			
: Sequence 8480, Application US/09396970			
: GENERAL INFORMATION:			
: APPLICANT: Gearling, David P.			
: APPLICANT: Kingsbury, Gillian A.			
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A			
: FILE REFERENCE: MN98-40PA			
: CURRENT APPLICATION NUMBER: US/09/396,970			
: CURRENT FILING DATE: 1999-09-14			
: EARLIER APPLICATION NUMBER: 60/100,293			
: EARLIER FILING DATE: 1999-09-14			
: NUMBER OF SEQ. ID NOS: 8756			
: SOFTWARE: FastSeq for Windows Version 3.0			
: SEQ ID NO 8480			
: LENGTH: 2564			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
: FEATURE:			
: NAME/KEY: misc_feature			
: LOCATION: (1)..(2564)			
: OTHER INFORMATION: n = A,T,C or G			
US-09-396-970-8480			

Query Match	95.28	Score 2150	DB 17	Length 2564
Best Local Similarly	99.48	Pred. No. 0		
Matches 2200	Conservative	0	Mismatches 10	Indels 4
				Gaps 4

Qy 25 ACCCTCAGCACAGCACACTCCCTTT-GGCAAGGACCTGAGACCCCTTGCTAAGTCAAGA 83
|||||
Db 50 accttcagcacagcacactccctltggcaagaacctgaacctgtgctaagtcaga 109

20 aaccgacacagcaccacccccccgagagacacccgagaccccccgcgcacacagccacagaa 107

QY	84	GGTCATATGGCTGCAGAAAGAACTAGAGAGACCAAGCAAAAGCCATGATATTTCATAG	143
Db	110	ggctcaatctggtctgagaagaactagagaagaaccaagaagccaatgatalttccatcg	169
QY	144	AAATGTCACAGACCCACAGGGGACCTTATGGAACATCTTTCACCTTGGGGGTCAGCAATG	203
Db	170	aaatgcagaagacaccaagaaggactatggaacacatcctaagctgtaggggtgagcaatg	229
QY	204	CTCTGTGTGGATTTTCCCTGGCACATCATGTGAACCTACTGCTGCACCTTACCATTTCTGAA	263
Db	230	ctctgtgtgattcttcctgtgcacatacctgaaaccgagctgtgacttaccatctctgaa	289
QY	264	AAACCCATGACTGGCAAAAGGCGCTAGAGAAATTCGCGGACAAATTTACACAGATTTAGTT	323
Db	290	aaacccatgaactctggcaaaaggctagaagattctgcggacaattacacagatttagt	349
QY	324	GGCATACAAAACAGGGCGGAAATTTAGATATCTTGAGGAAGACCTCTGCCCTTCACGTGCTTCT	383
Db	350	ggcatacaaaacaagaagcggaataatcgtagatctcggaagaagctctgccttccatcgcttct	409
QY	384	TACTACTGTGATAGAAATCCGGAAGATWAGAGAGAAATATGGACCTGGGTGGGAGCAACAAA	443
Db	410	tactactgtatgataatccggaaagatagaggaatactgagacgttgggtgggaaccacaaa	469
QY	444	TCTCTACTGAGAAAGACAGAAAGCTGGGAGATGCTGAGCCCAACACAGAAGAACAG	503
Db	470	tctcttactgaagaagcagagaccttgggaggttggtagcccaacaagaagaagaacag	529
QY	504	GAGGACCTGGCTGACATCTATTTCAAGAGAAACAAGATGCGAGCAATTTGACACATGAC	563
Db	530	gaggacctgggtggaatcctatcatalcaagaagaacaagaatgacgaaatgagaacgtagac	589
QY	564	CCCTCCCAACAACTTAAAGCACCCCTCTGTTCACAGCTTTCTTGGCACCCCTGGTCATGAC	623
Db	590	gctctgcacaacaactaaaggcagcctctgtctcacagcttctctgcagcctctggtcagtc	649
QY	624	AGTGGCCATGAGAAATGTGTAGAAATCATCAATTAATCACACCTGCACTGTGATGTGGGG	683
Db	650	agtggccatgagaatctgttagaaatcatalcaatacaccctgcgaactgtatgttgggg	709
QY	684	TTCATTGAGGGCCCCAGTGTACGCTTGTGATTCAGTGTGAGCCCTTGGAGGCCCAACCTG	743
Db	710	tactatgggccccagctgctagatcttggatcagctgtgagcctcttggagggccccagaagctg	769
QY	744	GGTACCATGAGACTGTACTACACCCCTTTTGGAACTTTCACCTTCAGCTCAGTGTGCTTC	803
Db	770	ggtaccacatgagactgtaccccaaccttgggaaacctcagcttcaagctcagctgtgctcttc	829
QY	804	AGCTGCTCTGAAGAACAACTTAACGTGGGATTTGAAGAAACCACTGTGGACCAATTTGGA	863
Db	830	agctgctctgaagaacaacttaactctgagatttgaagaaaccaactgtgagccatttggaa	889
QY	864	AACCTGCTATCTCCAGAACCAACCTGTCAAGTATTCAGTGTGAGCCTCTATCAGACCCA	923
Db	890	aaactgcatatctccagaaccaaacctgtcaagtgatcagctgtgagcctctacacagaccaa	949
QY	924	GATTTGGGGATCATAAACCTGTAGCCATCCCGCTGGCACCTTCACGCTTAAACCTTCACATG	983
Db	950	gatttggggatcataaacctgtatagccatccctgtgcacgcttcaagcttcaactctgtcaagtc	1009
QY	984	ACCTTCATCTGCTCGAAGAAAGAACTGATTAATTTGGGAAAGAAACCAATTTGTGTAATCA	1043
Db	1010	accttcacatctgctcgagaagaaactgtatatttgggaagaaabaaacatctgtgaatca	1069
QY	1044	TCTGGAATCTGTCAAAATCTTAGTCCAAATATGTCAAAAATTGGACAAAAGTTTCTCATG	1103
Db	1070	tctggaatctgtgtcaaaatctcttagctcacaatgttcaaaaatttgaacaaaagtttctcaatg	1129
QY	1104	ATTTAAGAGAGCGTGAATTAACCCCTCTTTCATTTCAGTGGGAGTCATGTTTACTGCATTC	1163
Db	1130	atttaagagaggtgtatataaacccctctctcatctccagctgagctcaatgtgttactgtcatctc	1189
QY	1164	TCTGGGTTGGCAATTATTCATTTTGGCTGTGCAGAGGATTTAAAAAAGGCAAGAAATCCAG	1223

Query Match	95.0%	Score 2146.8;	DB 36;	Length 2385;
Best Local Similarity	99.3%;	Pred. No. 0;		
Matches 2198;	Conservative 0;	Mismatches 12;	Indels 4;	Gaps 4
QY	ACCTGCAGACAGCAGCACTCCCTTTT-GGCAAGACCTGAGACCCCTTGTGCTGAAGTCAAGA	83		
Db				
	32 accctgcagacagcaacactccctcttggccaagaccctggacccttgcctgaagtcaga	91		
QY	84 GGCCTCAATGGGCTGCAGAGAACTAGAGAAGGAGCAAGCAAGCAACGCTGATATTTCATCG	143		
Db				
	92 ggctcaatggygcttgaagaagactagagaagagccaagccactgatacttcattg	151		
QY	144 AAATGTCAGACACCCAGAGGACTTATGGAACATTTCAAGTTGTGGGGTGGACAATG	203		
Db				
	152 aaatgtaagacacccacagaggaactatgtaacatcttaagtgtggyggygacaatg	211		
QY	204 CTCTGTTGTGATTTCTTGSCACATCATGTGAACCTACTGCTGSGACTTTACCATTTATTCGAA	263		
Db				
	212 ctctgtgtgattctctgacatactgaaacccagactgctgtaactacattatctgaa	271		
QY	264 AAACCCATGAACTGGGGAAGGCTTAGAGAAATTTCTGCCGAGCAATTTACAGATTTAGTT	323		
Db				
	272 aaacccatgtaacgycgaagggctagaagatctgcgagacaattacacagatttgc	331		
QY	324 GCCATCAAAACAAGCGGGAATTTAGTATCTGGAGAGACTCTGCCCTTCACTGCTTCT	383		
Db				
	332 gccatacaaaacaagcggaatgtagatcctggaggaagactctgccttcttaagtcgttct	391		
QY	384 TACTACTGATTAGGAATCCGGAAGTAGAGGAATATGAGAGTGGTGGGAGCAACCAAA	443		
Db				
	392 tactactggaataagataccggaagaatagaggaatlatggaagatggtgggaaccaca	451		
QY	444 TCTCTACAGGAAGCAGAGAACTGGGGAATGTGACGCCCAACAACAAGAAACAAG	503		
Db				
	452 tctcttactgaagaagcaggaactgggggagatgtgtgagccacaacaagaagaacag	511		
QY	504 GAGGACTCGGTGGAGATCTATATCAAGAAGAACAAATATCAGAGCAATATGACATGAC	563		
Db				
	512 gagagactcgtggaatctatatacaagaagaacaagaatgcaaggaatggaacgaatgac	571		
QY	564 GCGTCCCAACAACTAAAGGAGCCCTCTGTTCACAGCTTTTGGCCAGCTGTGTCATGCG	623		
Db				
	572 ggcctgcacaacaacaagaagcaccctctgttacaacagcttcttgcagccctggtc	631		
QY	624 AGTGGCATGAGAGATGTGAGAAATCAATCAATAAATCAACACTGCAACTGTGATGTTGGG	683		
Db				
	632 agtggcatgtgagaatgtgtagaataacatacaaatataacactggaactgtgattg	691		
QY	684 TACTATGGGCCCAAGTGTCACTTGTGATTCAGTGTGAGCCTTTGGAGGCCCGAGAGTG	743		
Db				
	692 tactatgagcccaagatcagatttggattcaggtgtgagcccttggagggccccaagactg	751		

OY	744	GGNACATGAGCATCTACTACACCCCTTTGGAAACTTCAAGCTTCAGCTCACAGTGTGCTTC	803
Db	752	ggtacacacgagctgactcaccccttgggaaacttcagcttcacagcagtgctccctc	811
OY	804	AGCTGCTCTGAAAGCAACAACCTTACCTGAGGATTTGAAACAACACCTGTGGACACTTTGGGA	863
Db	812	agcgctcttgaagaaacaaacttaacctgggatttgaagaacacccctggtgaccatttggaa	871
OY	864	AACTCGTCATCTCCAGAAACCAACCTGTCGAAGTGAATTCAGTGTAGGCTCTATTCAGCACCA	923
Db	872	aactgtcatctccagaaaccaactgtccaaagtattcagtgatgagctctatcagaacca	931
OY	924	GATTGGGGATCATGAACTGTAGCCATCCCTGGCCAGCTTCAGCTTTACTCTGCTATGT	983
Db	932	gatttgggatacgaagaaactgtagccatcccccctggccagcttcagcttaacctctgcatgt	991
OY	984	AACCTTCATCTGCTCAGAAAGAACCTGATTAATTTGGGAAGAAAGAAACCAATTTGTGAATGA	1044
Db	992	aacctcactctgctcagaagaaacggaattcaatctgggaagaagaacaaactctgtgaatca	1051
OY	1044	TCTGGAATCTGTCGTAATTCCTAGTCGAATATGTCAAAAAATTTGGACAAAAAGTTTCTCAATG	1104
Db	1052	tcgtgaatctggttcaaatccctagtcacatactgtccaaaaattgacaataaagtcttctcaatg	1111
OY	1104	ATTAAAGAGGGTGATTTATATACCCCTCTCATTTCCAGTGGCAGTCAATGGTTACTGCAATTC	1164
Db	1112	attaagaggagggtgatattataaccccctctcatccagtgagcagtcagtcatgttactgcatctc	1172
OY	1164	TCTGGGTTGGCAATTTATCAATTTGGCTGGCAGAGATTTAAAAAAGCGAAAGAAATCCAG	1224
Db	1172	tcctgggttggcaattatcatcatcttgctgtagcagaagatctaaaaaaggcagaagatccaaag	1231
OY	1224	AGAAGTATGAATGACCCCATATTAATATCGCCCTTGTCGTAAGAAATAATCTTTGGAAATCTTA	1283
Db	1232	agaagatgaatgaccccatatataatctgcctctggtgaaagaataattcttgaataactaa	1291
OY	1284	AAATCATGAGATCTCTTTAAATCTCTTCATGAANAAGTTTGTGTGTGGCAACCTCCTAGCT	1344
Db	1292	aaatcatgagatctctttaaactccctcccatgaagaagcttctgtgtgtagcaccctccatcagt	1351
OY	1344	CAAACTATGAAGCTGTG-TTCCGTCGATGTCATCTGGGAAGATTTCTACCCGACCAACAAGTTTC	1403
Db	1352	caaaactatgaagctgtctccctccatgtagcatctggtgaagatcttctaccgtgacacaagcttc	1411
OY	1403	CTTTCAGCTTCCAATTTCCGCCCTCATATTTATCCCTCAACCCCCAGCCCAAGAGCTTTATATC	1463
Db	1412	cttctcagcttccatcttgccctccatctatactccctcaaacccccagcccaacagtgcttatactc	1471
OY	1463	AGCTCAGCTTTTGTCTTTTCTGAGAGAAACAATAATAGACAT-ANAGGAAAGAGTTCA	1521
Db	1472	agctcagcttcttcttctcttcctgagggaaacaataatagacataaagggaagaagtatca	1531
OY	1522	TGTCGAATATTAAGATATGGCGACTTTGCTCTTTCTTGACTCTTTGTTTTCAGTTTCAATTC	1582
Db	1532	tgtcggaatataaagaatgagcgtgactctgctctctctcgtgactctgttcttaagcttcaatctc	1591
OY	1582	AGTCTCTTACCTTGATGACACACACTTTTAATGAAGCGCAAAATTTGATACATATATGGAAT	1641
Db	1592	agtgctcttactctgtagcagaacacctctctaaatgaagaatgcaaaattgtatcatcaatgtgaat	1651
OY	1642	ATGAGACTCAGTTTTCCTTGAGATCAAAATTTCAAGTGTGCTCTGTATTAAGTGTGGAGTAC	1701
Db	1652	atgagactcagtttctctctgtagcaataattcacaatcgtctctctctgtatactgtgagggatcc	1711
OY	1702	ACTCTTATAGAAAGTTTCAAAAAAGTCTAAGCTCTCTCTTTCTTAAGTCTCACTGGAAGTAA	1761
Db	1712	actcttatagaagaatctcaaaaaagctacgctctctctctcttcttaactcagtgaaatcaa	1771
OY	1762	TGGGGTCTCTGCTCAAGCTTGAAGAAGTCTTAATTTGGCACTGTAGGCTGTGGCTGTGAATTT	1822
Db	1772	tggggctctctcagagcttgaagaagctctatacttgcaacgttgagcctctgcgcctctgtgaatt	1831
OY	1822	GGACCATCTCTAATTTAACTGTGGCTTCAGGCGCTCCACACTTCTTTCAGGCACACTCTCTTTTTC	1881

Db	1832	gagacatcctatlttaaclygcttca-gcccccacacctctcagccacacctctcttcttc	1890
QY	1882	AGTTGGCTCACTTCCACACACTAGCATTCATGATGAGCGCCAGCAAAAGAGAGAAGAGAGA	1941
Db	1891	aglttgctgacttccacacctagcatlccacagatgcgaagcaagaagagagaagaga	1950
QY	1942	AATGACCTGCGGGTTTTTTAGTTTGGGGGTTTGTCTTTTCCTTTATGAGACCCATTC	2001
Db	1951	aatgacgctgctgttctttagttcttgagggtcttgctgttcttccctttagtgagccatctc	2010
QY	2002	CTATTTCCTTATAGTCAAGTCTTCTTTATCAGATATTATTATGTAAGAAACATCACTGA	2061
Db	2011	ctattctctatagtcatagttcttcttcaacgatatlatltagtgaagaaacatcaclyga	2070
QY	2062	AATGCGACTGCAAGGACATCTCTTTGATGTCATATGGAAGAGCTTAAACAGGTGAGGA	2121
Db	2071	aatgctagctgcaagtgacatctcttgatgcatatgagaaagatlaaacaaggtcgaga	2130
QY	2122	AATGCTTGTATTCACAGATGAATGCAATGCTTCCTTTCCCTCCGCCCGAGAACTTTATGCACT	2181
Db	2131	aattcttgatcttcaacaagaagtgtctctcttcttccctccgcgcacgaactttatccact	2190
QY	2182	TACCTAGATTTCTACATATTCTTTAAATTTGATCTCAGGCTTCCTCAACCCAC	2235
Db	2191	taccctagatctcacatcttctttaaattlcatlctcaggtccctccatcaacccac	2244
RESULT 7			
US-60-172-373-15742			
; Sequence 15742, Application US/60172373			
; GENERAL INFORMATION:			
; APPLICANT: Morris, Macdonald			
; APPLICANT: Lal, Preeti			
; APPLICANT: Diep, Dinh			
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using			
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polym			
; FILE REFERENCE: GX-0006 P			
; CURRENT APPLICATION NUMBER: US/60/172.373			
; CURRENT FILING DATE: 1999-12-16			
; NUMBER OF SEQ ID NOS: 25,772			
; SOFTWARE: PERL Program			
; SEQ ID NO 15742			
; LENGTH: 2387			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc_feature			
; OTHER INFORMATION: Incyte ID No: 331616.2			
US-60-172-373-15742			
Query Match			
Best Local Similarity 94.3%; Score 2129.6; DB 42; Length 2387;			
Matches 2201: Conservative 0; Mismatches 9; Indels 6; Gaps 6;			
QY	25	ACCTGACAGACA-GGACACTCCCTTT-GGCAAGGACGTGAGACCTTGTGTAACT-CAA	81
Db	32	accctgacagacagagacacacctcccttgggcaaggaccctggagcccttgctcaagctccaa	91
QY	82	GAGGCTCATAGGGGCTGCGAAGAACTAGAGAAGGNCNAAGCAAGCCATGATTTTTCAT	141
Db	92	gaggtcctaattggtcctgaggaagactagagaagacagaaagccatgatattcttcac	151
QY	142	GGAATGTCAGAGCACCAGAGGACTTATGCAACATCTTCAAGTTGTGGGGGTGACAA	201
Db	152	ggaatgtcagagacccacagagagactatgaaacatctcaagtctg9999t9gacaa	211
QY	202	TGCTGTGTTGTGATTTCTCGTGACATCATATGGAACCTACTGCTGGACATTAACATTATTCG	261
Db	212	tgcctctgtctgtatcttctctgacacatcaatggaaccgactgtgacttaccatattctcg	271
QY	262	AAAAACCATCAACTGCGAAGAGGCTAGAAAGATTCTGCGCGAGCAATTACACAGATTAG	321


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Db 272 aaaaaccctgaaactgcaaaaggtcagaagattctcgcgaagacaattacacagatttag 331
QY 322 TTGCCATACAAACAAAGCGGAAATTCGATCTCTGAGAAAGACTTCGCCCTTCAGTCTGTT 381
Db 332 ttgcatatacaaaacaaagcggaaatttgattctcgagaagactctgaccttcagtcgct 391
QY 382 CTTACTACTGATAGGAATCCGGAAGATAGGAGGAATATGAGCTGGGTGGGAACTCAACA 441
Db 392 cttaactactgataagataccggaagataaggaatatggaagctggtggtggaaccaca 451
QY 442 AATCTCTCAGTAAGAGCAGAGAACCTGGGAGATGTGAGCCCAACAAGAAAGAAC 501
Db 452 aatctctactcgaagaagcagagaactggggaagatggtagcccaacaagaagaaca 511
QY 502 AGGAGACTGCGCTGGAGATCTATATCAGAGAAACAAAGATGCAGGCAATGGAACGATG 561
Db 512 aggaagagactcgtgagatctatatacagaagaacaagaatgcaagcaaatggaagatg 571
QY 562 ACGCCCTGCCACAACCTAAAGGCAACCCCTCTGTACACAGCTTCTTGCCAGCCCTGTCAT 621
Db 572 acgcctgcacaacaactaaagacagccctctgttacacagctctctgcccagccctgcat 631
QY 622 GCAGTGGCCATGAGAGATGTAGAAATCATCAATCAATCAACCTGCACTGATGTGG 681
Db 632 gcaagtgccatggaagatgtagaataatcaataatcaactgcaactgtagatg 691
QY 682 GGTACTATGGGCCCGAGTCAAGCTTTCGATTCAGTGTGACCCCTTGGAGGCCCGAGAG 741
Db 692 ggtactatgagcccaagtgatgtagatgtagatgtagatgtagatgtagatgtagatg 751
QY 742 TGGGACCATGATGATCTGATCACCCTTTGAAACCTTCAGCTTCAGTTCAGTGTGCT 801
Db 752 tgggacacatgagactgtagatgtagatgtagatgtagatgtagatgtagatgtagatg 811
QY 802 TCAGTGTCTGAGAGAAACAACTTAACTGAGTTAGAGAAACCACTTGGAGCAATTTG 861
Db 812 tcaagctgctcgaaggaacaacttaactgggaatggaagaacacccctggaaccatttg 871
QY 862 GAACTGTGATCTCCGAGAACCACTGTCAAGTATGATGATGATGATGATGATGATGATG 921
Db 872 gaaactggtatctccagaacaactgtaagtgatgtagatgtagatgtagatgtagatg 931
QY 922 CAGATTTGGGATCATGAATCTAGCCATCCCTGCGCACTTCAGCTTACCTGTGAT 981
Db 932 cagatttgggatacgaactgtagcatccctggcagctcagcttcaactcctgcat 991
QY 982 GTACCTTCATGCTCAGAGAACTGAGTTAATTTGGAGAAAGAAACCACTTGTGAT 1041
Db 992 gtaccttcatctgcacagaagaactgagtttaattgggaagaagaacaacatctggaat 1051
QY 1042 CATCTGGAATCTGTCAATCTAGTCCATATGTCAAAAATTTGGACAAAGTTTGTCAA 1101
Db 1052 catctggaatctgtaaatctctgtaataatgtaaaatctggaacaagaattctcga 1111
QY 1102 TGATTAAAGAGGATATATATACCCCTCTTCATTTCCAGTGGCAGTCATGTTACGAT 1161
Db 1112 tgattaaagagggatataataacccctcttcattccagtgagcacaagttactgcat 1171
QY 1162 TCTCTGGGTGGCATTTATCATTTGGCTGGCAGAGATTTAAAAAAGGCAAGAAATCCA 1221
Db 1172 tctctgggttggcatattatcatttgcgcgaagagatlaaaaaaagcaagaatcca 1231
QY 1222 AGAAGCTATGATGAGCCCATATTAATGCCCCCTTGTTGAAAGAAATTTCTTGATGAT 1281
Db 1232 aggaagatagaaagcattataatcgccttggtagaagaataatcttgggaatct 1291
QY 1282 AAAAATCATGATCTTTAAATCTTCATGAGAAAGTTTGTGTGGTGACCTCTCTAC 1341
Db 1292 aaaaatcatagatctttaaactcttcaagaaagcgttctgtgtgtagaacctctac 1351
QY 1342 GTCAACATGAGATGTG-TTCTTATGTCATCTGGAGAGATTTCTCCAGCAACAGT 1400
Db 1352 gtcaaacatgagatgtagtcttccctcagtgatcctggaagaattctacatgcaaacagt 1411
QY 1401 TCTTTAGCTTTCCATTTTCGCCCTGCAATTTATCCCTCAACCCCGACAGCTGTTTAT 1460
Db 1412 tctttagcttccattctgcccctcaatctatccctcaaccccgccagcccaagtgcttat 1471
QY 1461 ACAGCTCAGCTTTTCTCTTTCTGAGAGAAACAAATTAAGCAT-TAAGGAAAGATTT 1519
Db 1472 acagctcagcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 1531
QY 1520 CATGTGGAATTAAGAGAGCTGACTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1579
Db 1532 catgtggaatataaagatagatgtagatgtagatgtagatgtagatgtagatgtagatg 1591
QY 1580 TCAGTGTGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1639
Db 1592 tcaagtgcttacttgatgtagatgtagatgtagatgtagatgtagatgtagatgtagatg 1651
QY 1640 ATATGACTCAGTTTCTGTCAGATCAATTTTCACTGCTGCTTCTGATGATGATGATG 1699
Db 1652 atatgactcagttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 1711
QY 1700 ACATCTTATGAAAGTTCAAAAAGTCTACGCTCTCTCTTCTTCTTCTTCTTCTTCTT 1759
Db 1712 acactctatagaagaagttcaaaaagctacgctctccttcttcttcttcttcttctt 1771
QY 1760 AATGGGCTCTGCTCAAGTTTGAAGAGTCTTATTTTTCAGCTGATGCTTCTGCTGTA 1819
Db 1772 aatgggctctgctcagtttgaagagtttcttcttcttcttcttcttcttcttcttctt 1831
QY 1820 TTGAGACATCTTATTTTAACTGCTTCAAGCCCTCCACCTTCTTCTTCTTCTTCTTCT 1879
Db 1832 ttgagacatcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 1890
QY 1880 TCACTTGTGCTGATTCACACTTACATCTGATGATGATGATGATGATGATGATGATG 1939
Db 1891 tcacttgtgctgacttccacactcagcactcactcactcactcactcactcactcactcact 1950
QY 1940 GAAATAGCCCTGGCGGTTTTTAACTTGGGGGTTTTTCTTCTTCTTCTTCTTCTTCTT 1999
Db 1951 gaaatagccctggcggtttttaaacttgggggttttcttcttcttcttcttcttcttctt 2010
QY 2000 TCTTATTTCTTATAGTCAATGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2059
Db 2011 tcttatttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 2070
QY 2060 GAAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2119
Db 2071 gaaatgctgactgactgactgactgactgactgactgactgactgactgactgactgact 2130
QY 2120 GAAATTCCTTGAATTCACAAATGAATGCTCTCCCTTCCCTGCCCCAGAACCTTTAT 2179
Db 2131 gaaatcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 2190
QY 2180 CTTACCTAGATTTCTACATATTTCTTAAATTTTCATCTCAGGCTCTCCCAACCC 2235
Db 2191 cttaaccagattctacatatctttaaattcaatctcaagctcctcccaaccacac 2246
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RESULT 8
PCT-US92-03970-1
Sequence 1, Application PC/TUS9203970
GENERAL INFORMATION:
APPLICANT: Dana-Farber Cancer Institute, Inc.
TITLE OF INVENTION: LEUKOCYTE-ASSOCIATED CELL SURFACE
NUMBER OF INVENTIONS: 1
TITLE OF INVENTIONS: PROTEIN
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Weingarten, Schurigin, Gagnebin & Hayes
STREET: Ten Post Office Square
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.

Db	1567	ACACCTCTAAATGAAGTGCAGAAATTTGGATACATATATGTGAATATGGACACGATTTTCTTGCA	1626
QY	1662	GATCAAAATTCACGTGCTGCTCTTGATATCTGGAGGTACACTCTTATGAAGTTCAAA	1721
Db	1627	GATCAAAATTCGGGTGCTCTTGATATAC-GTGGAGGTACACCT-----ATGAAGTCAA	1680
QY	1722	AAGCTACGCTCTCTCTTCTTTCTTACACAGTGAATATGGAGTCCGCTGCAAGTTGA	1781
Db	1681	AAGCTACGCTCTCTCTTCTTTCTTACCTCAGTGAATATGGAGTCTGCTCAAGTTGA	1740
QY	1782	AAGAGTCATATTGGACTAGTAGCCGCGCGCTGTGAATTTGACATCCTATTACTGG	1841
Db	1741	AAGAGTCATATTGGACTAGTAGCCGCGCTGTGAATTTGACATCCTATTACTGG	1800
QY	1842	CTTCAGGCTCCCAACCTTCTTCAGCCACCTCTTTTCAGTGGCTGCACTTCACACC	1901
Db	1801	CTTCA-GCCTCCCACTCTTCTTGAGCACTCTCTTTTCAGTGGCTGCACTTCACACC	1859
QY	1902	TAGCATCTCATGAGTGGCAAGCAAAAAGAGAGAGAAATAGCCGCGCGGTTTTT	1961
Db	1860	TAGCATCTCATGAGTGGCAAGCAAAAAGAGAGAGAAATAGCCGCGCGGTTTTT	1919
QY	1962	AGTTGGGGGGTTTGTCTTTCTTTTATGAGACCCATTCTCTATTCTTATAGTCANGT	2021
Db	1920	AGTTGGGGGGTTTGTCTTTCTTTTATGAGACCCATTCTCTATTCTTATAGTCANGT	1979
QY	2022	TTCCTTATACCAATATATATAGTAAGAAAACATCACTGAATAGCTAGCGCAAGTGCA	2081
Db	1980	TTCCTTATACCAATATATATAGTAAGAAAACATCACTGAATAGCTAGCGCAAGTGCA	2039
QY	2082	TCTCTTGATGATCATATGAAAGTTAAACAGTGGAGAAATTCCTTGATTCACAAATGA	2141
Db	2040	TCTCTTGATGATCATATGAAAGTTAAACAGTGGAGAAATTCCTTGATTCACAAATGA	2099
QY	2142	AATGCTCTCTTCCCTGCCCCAGAACTTTATCAGTACTAGTATCTACATATTC	2201
Db	2100	AATGCTCTCTTCCCTGCCCCAGAACTTTATCAGTACTAGTATCTACATATTC	2159
QY	2202	TTTAAATTCATCTAGGCGTCCCTCAACCCAC	2235
Db	2160	TTTAAATTCATCTAGGCGTCCCTCAACCCAC	2193

RESULT 9
ECT-US94-00909-1
Sequence 1, Application PC/TUS9400909
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS BLOCKING
TITLE OF INVENTION: AGENTS FOR COMPONENT SELECTIN FUNCTION
NUMBER OF SEQUENCES: 11
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00909
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,606
FILING DATE: 30-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/962,483
FILING DATE: 02-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,608
FILING DATE: 03-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/737,092
FILING DATE: 29-JUL-1991

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? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/730,503
? FILING DATE: 08-JUL-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/700,773
? FILING DATE: 15-MAY-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/313,109
? FILING DATE: 21-FEB-1989
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2330 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? HYPOTHEetical: NO
? ANTI-SENSE: NO
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 53..1210
PCT-US94-00909-1

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Query Match	92.48%	Score 2087.6;	DB 1;	Length 2330;
Best Local Similarity	98.58%	Pred. No. 0;		
Matches 2161; Conservative	0;	Mismatches	24;	Indels 9; Gaps
QY 44	CCCTTTGGCAAGACCTGAGACCTTGTGTGCTAAGTCAAGAGGCTCAATGSGCTGCAGAAAG	103		
Db				
7	CCCTTTGGCCAAAGACCTGAGACCTTGTGTGCTAAGTCAAGAGGCTCAATGSGCTGCAGAAAG	103		
QY 104	AACATAGAAAGGACCAAGCAAAAGCCATGATATTTTCATGTGAATATGTCAAGCAACCCAGAG	66		
Db				
67	AACATAGAAAGGACCAAGCAAAAGCCATGATATTTTCATGTGAATATGTCAAGCAACCCAGAG	163		
QY 164	GCACATTATGGAACATCTTCAAGTTGTGGGGGTGAGACATCTCTGTGTGATTTCTGTGC	223		
Db	127	GGACATTATGGAACATCTTCAAGTTGTGGGGGTGAGACATCTCTGTGTGATTTCTGTGC	186	
QY 224	ACATCATGGAACCTACATGCTGGGACTTACCTATTTCTGTGA AAAAACCATGTAACGTGCAAG	283		
Db	187	ACATCATGGAACCCACATGCTGGGACTTACCTATTTCTGTGA AAAAACCATGTAACGTGCAAG	246	
QY 284	GGCTAGGAAGATTTCTGCCGAGACAATTATACAGATTTAGTTGGCATACAAACAAAGGGGGA	343		
Db	247	GGCTAGGAAGATTTCTGCCGAGACAATTATACAGATTTAGTTGGCATACAAACAAAGGGGGA	306	
QY 344	AATTGAGTATCTGAGAGAAGACTGTGCCCTTCAGCTGTTCTTACTAGTGAGGAATCCG	403		
Db	307	AATTGAGTATCTGAGAGAAGACTGTGCCCTTCAGCTGTTCTTACTAGTGAGGAATCCG	366	
QY 404	GAGGATTAGGAGGATTTATGACGTGGGTGGGAACCAACAAATCTCTCACTAGAGAGCAAG	463		
Db	367	GAGGATTAGGAGGAAATATGACGTGGGTGGGAACCAACAAATCTCTCACTAGAGAGCAAG	426	
QY 464	GAACCTGGGAGATGTTGAGGCCCAACAACAACAAGAGAGACTCGCTGGAGATCTA	523		
Db	427	GAACCTGGGAGATGTTGAGGCCCAACAACAACAAGAGAGACTCGCTGGAGATCTA	486	
QY 524	TATCAAGAAACCAAGATGCAAGCCAAATGGAAGATGAGCCCTGCGCAACCTAAAGGC	583		
Db	487	TATCAAGAAACCAAGATGCAAGCCAAATGGAAGATGAGCCCTGCGCAACCTAAAGGC	546	
QY 584	AGCCCTCTGTTACACAGCTTCTTCCAGGCCCTGGTATGAGTGGCCATGAGGAATGTGT	643		
Db	547	AGCCCTCTGTTACACAGCTTCTTCCAGGCCCTGGTATGAGTGGCCATGAGGAATGTGT	606	
QY 644	AGAAATATCAATATATACACCTGCAACTGTGATGTGGGGTACTATGGGCCCCAGTGTCA	703		
Db	607	AGAAATATCAATATATATACCTGCAACTGTGATGTGGGGTACTATGGGCCCCAGTGTCA	666	
QY 704	GCCTGTGATTTCAGTGTGAGCCCTTTGGAGGCCCCAGAGCTGGGGTACCATGACACTGTACTCA	763		

Query Match	92.48;	Score 2087.6;	DB 4;	Length 2330;
Best Local Similarity	98.58;	Pred. No. 0;		
Matches 2161;	Conservative	0;	Mismatches 24;	Indels 9;
				Gaps 5;

2

Db	607	AAATAATCATCATTAATTATTAACCTGCAACCTGTGATGTGGGGATCTATGTGGGCCCAAGTGTCA	666
QY	704	CGTTGTGATTCAGTGTGAGCCCTTTGGAGGCCCCAGAGCGTGGGTATCAATGACCTGTACTCA	763
Db	667	GTTTGTGATTCAGTGTGAGCCCTTTGGAGGCCCCAGAGCGTGGGTATCAATGACCTGTACTCA	726
QY	764	CCCCCTTTGGAAACTCTCAAGCTTTCAGCTTCACAGTGTGCTTTCAAGCTGTCTGTGAAGAACAA	823
Db	727	CCCTTTGGGAAGACTCAACTCTCAACTCAACAGTGTCCCTTCAGCTGTCTGTGAAGAACAA	786
QY	824	CTTAACHTGGGATTTGAAGAAACCAACCTGTGGACCAATTTGAAACAGTGCATCTCCAGAAC	883
Db	787	CTTAACHTGGGATTTGAAGAAACCAACCTGTGAACCAATTTGAAACAGTGCATCTCCAGAAC	846
QY	884	AACCTGTCAAGTATTCACGTGTGTGAGCTCTATACAGCACACAGATTTGGGGATCATGTAACTG	943
Db	847	AACCTGTCAAGTATTCACGTGTGTGAGCTCTATACAGCACCAATTTGGGGATCATGTAACTG	906
QY	944	TAGCATCCCTCGCCAGCTTCACAGCTTACCTCGTCGATGTACCTTCATCTGTCTCAGAAAG	1007
Db	907	TAGCATCCCTCGCCAGCTTCACAGCTTACCTCGTCGATGTACCTTCATCTGTCTCAGAAAG	966
QY	1004	AACCTGATTAATTGGGAGAGAGAAACCAATTTGTAATCATCTGTGAATCTGTGCAATCTC	1065
Db	967	AACCTGATTAATTGGGAGAGAGAAACCAATTTGTAATCATCTGTGAATCTGTGCAATCTC	1022
QY	1064	TAGTCCAAATGTGTCAAAAATTTGGACAAAAGTTTCCAAATGATTAAGGAGGTGATTAATA	1122
Db	1027	TAGTCCAAATGTGTCAAAAATTTGGACAAAAGTTTCCAAATGATTAAGGAGGTGATTAATA	1086
QY	1124	CCCCCTCTTCATTCACAGTGGCAGTCAATGTACTCAATCTCTGTGGGTGGCAATTAATCAT	1183
Db	1087	CCCCCTCTTCATTCACAGTGGCAGTCAATGTACTCAATGTCTGTGGGTGGCAATTAATCAT	1146
QY	1184	TTGGCTGTGGGAAGAGAGATTAAAAAAGGCAAGAATCCAAAGAAAGTATGAATAGACCATA	1243
Db	1147	TTGGCTGTGGGAAGAGAGATTAAAAAAGGCAAGAATCCAAAGAAAGTATGAATAGACCATA	1206
QY	1244	TTTAATGCGCCCTGTGTGAAAGAAAAATTTCTGGAATACTAAAAATCATGTAGATCTTTAAA	1303
Db	1207	TTTAATGCGCCCTGTGTGAAAGAAAAATTTCTGGAATACTAAAAATCATGTAGATCTTTAAA	1266
QY	1304	TCCCTTCATGAAGAAGTTTGTGTGTGTGGCACTCTACGTCACAAACATGAAGTGTG-TTCC	1362
Db	1267	TCCCTTCATGAAGAAGTTTGTGTGTGTGGCACTCTACGTCACAAACATGAAGTGTGTTC	1326
QY	1363	TTTCAGTGCATCTGGGAGAGATTTCTACCCGACCAACAGTTCTTCACACTCCATTTTCGGCC	1422
Db	1327	TTTCAGTGCATCTGGGAGAGATTTCTACCTGACCAACAGTTCTTCACACTCTTCACACC	1386
QY	1423	CTTCATTTATCCCTCAACCCCGACGCCACAGGTGTTTATACACTGAGCTTTTGTCTTTT	1482
Db	1387	CTTCATTTATCCCTCAACCCCGACGCCACAGGTGTTTATACACTGAGCTTTTGTCTTTT	1446
QY	1483	CTGAGAGAAACAAATTAAGACAT-TAAGGAAAGATTCATGTGAATATTAAGATGCT	1541
Db	1447	CTGAGAGAAACAAATTAAGACATTAAGGAAAGATTCATGTGAATATTAAGATGCT	1506
QY	1542	GACCTTGTCTCTTCTTGTGACGTCTGTGTTTCAAGTTCAATTCAGTGCCTGTACTTGTATGACAG	1601
Db	1507	GACCTTGTCTCTTCTTGTGACGTCTGTGTTTCAAGTTCAATTCAGTGCCTGTACTTGTATGACAG	1566
QY	1602	ACACTCTTAATTAAGAGCAAAATTTGATACATATGTGAATATGAGACATGATTTTCTTGCA	1661
Db	1567	ACACTCTTAATTAAGAGCAAAATTTGATACATATGTGAATATGAGACATGATTTTCTTGCA	1626
QY	1662	GATCAAAATTTACGTCGCTCTCTGTATGTACTGTGAGAGTACACTCTTATTAAGAAATGTTCA	1721
Db	1627	GATCAAAATTTACGTCGCTCTCTGTATGTACTGTGAGAGTACACTCTTATTAAGAAATGTTCA	1680
QY	1722	AAGTCTACGCTCTCTTCTTCTTAACCTCACTGAAGTATATGTGGGCTCGCTGCAAGTTGA	1781
Db	1681	AAGTCTACGCTCTCTTCTTCTTAACCTCACTGAAGTATATGTGGGCTCGCTGCAAGTTGA	1740

Qy	1782	AAGAGTCCTATTGGACACTGTAGAGCTGGCCGTCGTGTAATTGGACCATCTTAATTAACTGG	184.1
Dp	1741	AAGAGTCCTATTGGACACTGTAGAGCTGGCCGTCGTGTAATTGGACCATCTTAATTAACTGG	180.0
Qy	1842	CTTAGAGCCTCCACACCTTCTTAGACCACTCTCTTTTCAGTGGCTGACTTCCACACC	190.1
Dp	1801	CTTACA-CCGTCGCCACACTCTTCTTAGACCACTCTCTTTTCAGTGGCTGACTTCCACACC	185.9
Qy	1902	TAGCATCTCATGTAGAGTGGCCAAGAAAAGAGAGACAGAGAAATAGCCGTCGCCGCTTTTCTT	196.1
Dp	1860	TAGCATCTCATGTAGAGTGGCCAAGAAAAGAGAGAGAAATAGCCGTCGCCGCTTTTCTT	191.9
Qy	1962	AGTTGGGGGTTTTCGCTTCTCTTTATGAGACCATTCTTAATTCTTAATGATCATGT	202.1
Dp	1920	AGTTTGGGGGTTTTCGCTTCTCTTTATGAGACCATTCTTAATTCTTAATGATCATGT	197.9
Qy	2022	TTCTTTATGACGATATTATTATAGTAAGAAACATCACTGAATGCTAGCTGCAAGTGGACA	208.1
Dp	1980	TTCTTTATGACGATATTATTATAGTAAGAAACATCACTGAATGCTAGCTGCAAGTGGACA	203.9
Qy	2082	TCCTCTTTCATGTCTCATGTGAAGAGTTAAAAACAGAGTGGAGAAATTCCTTGATTTACAAATGA	214.1
Dp	2040	TCCTCTTTCATGTCTCATGTGAAGAGTTAAAAACAGAGTGGAGAAATTCCTTGATTTACAAATGA	209.9
Qy	2142	AATGCTCTCCTTTCCCTCCGCCCCAGACACTTTTATTCACATTACTAGATTCATATTC	220.1
Dp	2100	AATGCTCTCCTTTCCCTCCGCCCCAGACACTTTTATTCACATTACTAGATTCATATTC	215.9
Qy	2202	TTTAAATTTATCTGACAGGCTCCCTTAACCCAC	223.5
Dp	2160	TTTAAATTTATCTGACAGGCTCCCTTAACCCAC	219.3

RESULT 11
 US-08-340-539-1
 Sequence 1, Application US/08340539
 GENERAL INFORMATION:
 APPLICANT: Tedder, Thomas F.
 APPLICANT: Kansas, Geoffrey S.
 TITLE OF INVENTION: CHEMERIC SELECTINS AS SIMULTANEOUS
 TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
 STREET: Ten Post Office Square
 City: Boston
 STATE: MA
 COUNTRY: USA
 Zip: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/340,539
 FILING DATE: 16-NOV-1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/008,459
 FILING DATE: 25-JAN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/983,606
 FILING DATE: 30-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/862,483
 FILING DATE: 02-APR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/770,608
 FILING DATE: 03-OCT-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/737,092

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1      FILING DATE: 29-JUL-1991
2      PRIOR APPLICATION DATA:
3      APPLICATION NUMBER: US 07/730,503
4      FILING DATE: 08-JUL-1991
5      PRIOR APPLICATION DATA:
6      APPLICATION NUMBER: US 07/700,773
7      FILING DATE: 15-MAY-1991
8      PRIOR APPLICATION DATA:
9      APPLICATION NUMBER: US 07/313,109
10     FILING DATE: 21-FEB-1989
11     ATTORNEY/AGENT INFORMATION:
12     NAME: Heine, Holliday C.
13     REGISTRATION NUMBER: 34,346
14     REFERENCE/DOCKET NUMBER: DDCI-318XX
15     TELECOMMUNICATION INFORMATION:
16     TELEPHONE: (617) 542-2290
17     TELEFAX: (617) 451-0313
18     TELEX: 940675
19     INFORMATION FOR SEQ ID NO: 1:
20     SEQUENCE CHARACTERISTICS:
21     LENGTH: 2330 base pairs
22     TYPE: nucleic acid
23     STRANDEDNESS: single
24     TOPOLOGY: linear
25     MOLECULE TYPE: cDNA
26     HYPOTHEICAL: NO
27     ANTI-SENSE: NO
28     FEATURE:
29     NAME/KEY: CDS
30     LOCATION: 53..1210
31     PUBLICATION INFORMATION:
32     DOCUMENT NUMBER: US 07/700,773
33     FILING DATE: 15-MAY-1991
34     US-08-340-539-1

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[illegible]

Db	487	TATCAAGAGAAACAAGATGAGGCAATATGAAAGATGAGCCGCCCAAACTAAAGGC	546
Oy	584	AGCCCTCTGTTACACACCTTCTTGCCAGCCCTGGTCAATGCAAGTGGCCATAGAAATGTG	643
Db	547	AGCCCTCTGTTACACACCTTCTTGCCAGCCCTGGTCAATGCAAGTGGCCATAGAAATGTG	606
Oy	644	AGAAATCATATATATACACACCTGCAACCTGTGATGTGGGTACTATATGGCCCACTGTCA	703
Db	607	AGAAATCATATATATATACACACCTGCAACCTGTGATGTGGGTACTATATGGCCCACTGTCA	666
Oy	704	GCATTGATTCAGTGTGAGCCCTTTGAGAGGCCCAAGCTGGGTACCATGAGTGTACTCA	763
Db	667	GTTTGTGATTCAGTGTGAGCCCTTTGAGAGGCCCAAGCTGGGTACCATGAGTGTACTCA	726
Oy	764	CCCTTTGGAAATCTGAGCTTCAGCTCACAGTGGCTTCACTGCTCTGAAAGAACAA	823
Db	727	CCCTTTGGAAATCTGAGCTTCAGCTCACAGTGGCTTCACTGCTCTGAAAGAACAA	786
Oy	824	CTTTAACTGGGATTGAAGAAACACCTGTGGACATTTTGGAACTGGTCAATCCGAAC	883
Db	787	CTTTAACTGGGATTGAAGAAACACCTGTGGACATTTTGGAACTGGTCAATCCGAAC	846
Oy	884	AACTGTCAAGGATTTCAGTGTGAGCCCTATACACACCACAGTTTGGGATCAGTCACTG	943
Db	847	AACTGTCAAGGATTTCAGTGTGAGCCCTATACACACCACAGTTTGGGATCAGTCACTG	906
Oy	944	TAGCCATCCCTGGCCAGCTTACGTTTACCTGTGATGATCCCTCATCTGTCAAGAG	1003
Db	907	TAGCCATCCCTGGCCAGCTTACGTTTACCTGTGATGATCCCTCATCTGTCAAGAG	966
Oy	1004	AACTAGTTTAAATGGGAGAAAGAACCATTTGGAATCAATCTGGAATCTGTCAATCC	1063
Db	967	AACTAGTTTAAATGGGAGAAAGAACCATTTGGAATCAATCTGGAATCTGTCAATCC	1026
Oy	1064	TAGTCCAAATATGTCAAAAATTTGGACAAAAGTTTCTCATGTATTAAGAGGGTGATTTAA	1123
Db	1027	TAGTCCAAATATGTCAAAAATTTGGACAAAAGTTTCTCATGTATTAAGAGGGTGATTTAA	1086
Oy	1124	CCCCCTCTTCATCCAGTGGGAGTCAATGTTTACGCACTCTGTGGTTGGCATTTATCAT	1183
Db	1087	CCCCCTCTTCATCCAGTGGGAGTCAATGTTTACGCACTCTGTGGTTGGCATTTATCAT	1146
Oy	1184	TTGGCTGGCAAGAGATTTAAAAAAGGACAGAAATCCAAAGAGATGAATGACCATA	1243
Db	1147	TTGGCTGGCAAGAGATTTAAAAAAGGACAGAAATCCAAAGAGATGAATGACCATA	1206
Oy	1244	TTAAATGGCCCTGTGTCAAAGAAATTTCTTGGAATCTAAAAATTCAGATCCTTTAA	1303
Db	1207	TTAAATGGCCCTGTGTCAAAGAAATTTCTTGGAATCTAAAAATTCAGATCCTTTAA	1266
Oy	1304	TCTCTTCATGAAACGTTTGTGTGGTGGGACGCTCCAGTGCAAACATGAAAGTGTG-TTCC	1362
Db	1267	TCTCTTCATGAAACGTTTGTGTGGTGGGACGCTCCAGTGCAAACATGAAAGTGTGTTC	1326
Oy	1363	TTTAGTGGCAATGGGAGAGTTTCTACCCGACAAACAGTTCCTTCAGCTTCCATTTGACC	1422
Db	1327	TTTAGTGGCAATGGGAGAGTTTCTACCCGACAAACAGTTCCTTCAGCTTCCATTTGACC	1386
Oy	1423	CTCATTTATCCCTCAACCCCAAGCCACAGTGGTTTATACACCTGAGCTTTTGTCTTTT	1482
Db	1387	CTCATTTATCCCTCAACCCCAAGCCACAGTGGTTTATACACCTGAGCTTTTGTCTTTT	1446
Oy	1483	CTGAGAGAGAAATAATAGACCAT-ATAGGGAAGAGTTCATGTGGATATATAAGATGGCT	1541
Db	1447	CTGAGAGAGAGAAATAATAGACCAT-ATAGGGAAGAGTTCATGTGGATATATAAGATGGCT	1506
Oy	1542	GACCTTGTCTTTCTTGGAGCTCTGTGTTTCAGTTTCAATTCAGTGTGTGATGTGACAG	1601
Db	1507	GACCTTGTCTTTCTTGGAGCTCTGTGTTTCAGTTTCAATTCAGTGTGTGATGTGACAG	1566
Oy	1602	ACACTTCTTAATGAAGTCAAAATTTGATACATATATGTGATATGAGTCACTTCTTGCA	1661

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Db      1567 AACCTTCAAAATGACGTGCAAAATTGGTAATCATATGTCGAATATGAGACTACGATTTTCTTGCA 1626
QY      1662 GATCAAAATTTCCAGTGCATCTTCTGTATACGTGGAGGAGACACTTATATGAAGATTCAA 1721
        |||||||
Db      1627 GATCAAAATTTCCAGTGCATCTTCTGTATAC - GTGGAGGTACACTCT-----ATGAAGTCAA 1680
QY      1722 AAGCTTCAGCTCCTCTTCTTCTTCTTAACCTCAGTGAAGTAATGGGAGTCCGTCAAGTTGA 1781
        |||||||
Db      1661 AAGCTTCAGCTCCTCTTCTTCTTCAACCTCAGTGAAGTAATGGGAGTCCGTCAAGTTGA 1740
QY      1782 AAGAGTCCATTTTGGCACTAGCTCGGCCGTGCTGATATGGACCATCTATTTACTGG 1841
        |||||||
Db      1741 AAGAGTCCATTTTGGCACTAGCTTAGCTCGGCCGTCTGTGATTTGACAATCTTATTTAACYG 1800
QY      1842 CTTAGAGCTCCCCACCTTCTTTCAGCACACCTCTCTTTTTCAGTGGACTGACTCCACACC 1901
        |||||||
Db      1801 CTCTCA - GCCCTCCCACCTCTTTCAGCACACCTCTCTTTTCAGTGGACTGACTCCACACC 1859
QY      1902 TACGATCTCATGATAGAGGCCACAGCAAAAAGAGACAGAAGACAATAATACCTCGCCGCTTTTTT 1961
        |||||||
Db      1860 TAGACTCTCATAGTAGGCCAACAGAAAGAGAGAGAAATAATACCTCGCCGCTTTTTT 1919
QY      1962 AGTTTGGGGCTTTTCTGTCTTCTTATAGACCCATCTCATTTTCTTATAGCAATGT 2021
        |||||||
Db      1920 AGTTTGGGGCTTTTCTGTCTTCTTATAGACCCATCTCATTTTCTTATAGCAATGT 1979
QY      2022 TTCTTTTATCAGATATATATAGTAAGAAAAACATCATGAAATGCTAGCTGCAAGTGACA 2081
        |||||||
Db      1980 TTCTTTTATCAGATATATATATAGTAAGAAAAACATCATGAAATGCTAGCTGCAAGTGACA 2039
QY      2082 TCTCTTTCATGTCATATATGGAAGATTAAAAAGGTGAGAAATTCTTGATATACAAATGA 2141
        |||||||
Db      2040 TCTCTTTCATGTCATATATGGAAGATTAAAAAGGTGAGAAATTCTTGATATACAAATGA 2099
QY      2142 ATATGCTCTCTTCCCTGCCCCCAGAACCTTTTATCAGTACTAGATATCTACATATTC 2201
        |||||||
Db      2100 AATGCTCTCTTCCCTGCCCCCAGAACCTTTTATCAGTACTAGATATCTACATATTC 2159
QY      2202 TTTAAATTTCAATCAGAGCTCTCCCTCAACCCAC 2235
        |||||||
Db      2160 TTTAAATTTCAATCAGAGCTCTCCCTCAACCCAC 2193

RESULT 12
US-08-410-569-1
; Sequence 1, Application US/08410569
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; APPLICANT: Sperlnt, Olivier G.
; TITLE OF INVENTION: LEUKOCYTE ADHESION MOLECULE-1 (LAM-1)
; NUMBER OF INVENTION: AND LIGAND THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,569
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA.
; APPLICATION NUMBER: US 07/770,608
; FILING DATE: 03-OCT-1991
; APPLICATION NUMBER: US 07/700,773
; FILING DATE: 15-MAY-1991

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RESULT 14
US-60-164-285-5456
; Sequence 5456, Application US/60164285
; GENERAL INFORMATION:
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Tumor Associated Molecules (TAMS): Targets for diagnosis, treatment
; FILE REFERENCE: 3214
; CURRENT APPLICATION NUMBER: US/60/164,285
; CURRENT FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 8259
; SEQ ID NO 5456
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-164-285-5456

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Query Match	71.1%	Score 1605.4	DB 41	Length 1788
Best Local Similarity	99.48%	Pred. No. 0		
Matches 1653; Conservative	0	Mismatches	6	Indels 4; Gaps 4;

QY	576	CTAAGGAGAGCCCTCTGTACACAGCTTCTTCCAGCCCTGTATATGACAGTGGCATGGA	635
Db	1	ctlaaaagagccctctgtltaacacagctctcttgcagcccttgtacltgagltggccaatgga	60
QY	636	GAATGTGTGAATCATCATTAATATCACACCTGCACACTGTGATGTGGGTACTATGGGCC	695
Db	61	gaatgtgtgaaatcatcatatcaataatlaacacccctgcacacttgatgttgggtactatbggcc	120
QY	696	CAGTGTACGCTTGTGATTCAGTGTGAGCCCTTTGAGGCCCCAGAGCTGGGTACCATGAGC	755
Db	121	cagtgtcagctgtgtatctcagltgagtcctcttgagagccccagactgltgataccatgagc	180
QY	756	TCTACTACCCCTTTGGAAACTTCAGCTTCAGCTACAGTGTGGCTTACGCTGCCTTAA	815
Db	191	tgtaactacccctcttggaaacttcagcttcagctcacagltgtccctlaagctgtcctgaa	240
QY	816	GGAAACAATTAACAGGGGATGTGAAGAACCAACTGTGACCAATTTGGAAACTGGGCATCT	875
Db	241	ggaaacaacttaactcgggaaatctgaagaacaacacctgtgacacatcttggaaactgtgcac	300
QY	876	CCAGAACCAAGCTGTCAAGTGAATGATGTAGTGAAGCCCTCATGACACCAAGATTTGGGGATC	935
Db	301	ccagaaaccaactcgtgcaagtgatctcagltgtgagccctctacagcacccagatcttgggagtc	360
QY	936	ATGAACCTTACCGCAATCCCTCGGCCAG-CTTCAGCTTTACCTCTGTGATGTACCTTCATCTG	994
Db	361	atgaacctgtaaagccatccccctcggccagccctcagactcttaccctctgaaatgtacctatctt	420
QY	995	CTCAGAAAGAACTGAGTTAATTTGGAGAGAAAGAAACATTGTGTGATCATCTGGAATCTG	1054
Db	421	ctcagaaagaaactgagttcaatcttggagaagaagaaaccccttctgtgaatcaatcttggaa	480
QY	1055	GTCAAATCCTAGTCCAAATATGTCAAAAATTTGACAAAGTTTCTCAATGATTAAGAGAGG	1114

D	481	gctaaatccctagctccaatatactgcaaaaattggcgaaaaagctttctcaatgatactaaagagag	540
Q	1115	tgattatTAACCCCGCTTTCAATTCACAGTGGCAGTGGTACTGCAATTCCTGCGGGTGGC	1174
D	541	tgattataaaccctctctcatctccagtcgagcactgattactgcatactctcgggtctgc	600
Q	1175	ATTATCAATTTGGCTGGCAGGAGATTTAAAAAAGCAGAAATCCAGAGAAAGTATGA	1233
D	601	attctcaatttgctggtgcaagagatctaaaaaaaaggcaaaatctcaagagaaatgata	660
Q	1235	tgACCATATTAATTCGCCCTTGCTGTAAGAAATAATTTCTTGAAATACTTAAATTCATGGA	1294
D	661	tgaccacatactaaatctgcctctggctgaagaagaaatctctggaaactactaaaaatcattgga	720
Q	1295	TCCTTTAAATCCTTTCATGGAACGTTTGTGTGGACCCCTCCATACGTCAACATGAAG	1354
D	721	tcctttaaactccctccatctgaagaagctttgtgtgtgtgagaccctccatcagtcacaaatagag	780
Q	1355	TGTG-TTCCCTTCACTGCATCTGGAGAGATTTCTAACCCGACACACAGTTCCCTTCACTTCC	1413
D	781	tgctttcccttcagtcgatactcggaaagattctcaactcgacaaacagttccctccagctcc	840
Q	1414	ATTTCGGCCCGCATTTTTCCTCAACCCCGACCGCACAGTGGTTTATACAGTCAGCTTT	1473
D	841	atttcgcccctccattctaccctcaaccccccagcccaagtgattctaaagctccagctt	900
Q	1474	TTTGCTTTTCTGAGACAGAAACAATAAGACCAT-AAGGGAAAGCATTCATCTGCAATTA	1532
D	901	ttgtctttctcggagggagaaacaaataagaccataaagggaagaagattcaatctcgtggaata	960
Q	1533	AAGATGCTGACTTTCCTTTCTTGACCTGTGTTTTCAAGTTTCAATTCACTGCTGACT	1592
D	961	aagaatgctgactctgctctctctctcgtcctctgtttctcagttcaatctcagtcgctact	1020
Q	1593	TGATGACGACACTTTTCAATGAAGGCCAAATTTGATACATATGTGAATATGACTACT	1652
D	1021	tgatgacgacaactctcaaaagaagtgcaaatctcgatactatgtgaaatactgactagct	1080
Q	1653	TTTTCTTGAGATCAAAATTTTACAGTGGCTTCTGTATACGTGGAGTACACTTATAGA	1712
D	1081	ttctcttgagatccaattctcaagctcgtctctctgtataactcgtggagtgaaactctataga	1140
Q	1713	AAGTTCAAAAAGTCTACGCTCTCTTTCTTCTTAACCTCAGTGAAGTAATGGGCTCTGC	1772
D	1141	aagttcaaaaagctcactgactcctctctctctctcaactcagtgaaatggtgctctgc	1200
Q	1773	TCAGATTGAAGACTCCTATTTTGACAGTGAAGCTCGCCGCTGTGTAAATTTGAGCAATCCTA	1832
D	1201	tcgaattgaaagaagctctattctgaactgtaactcgtcgtctgtgaaattggaaccctcta	1260
Q	1833	TTTTAAGTGGCTTTCAGGGCTCCCGACCTTCTTTCAGCCACTCTCTTTTTCAGTTGGCTAC	1892
D	1261	tttaactcgtgctca-gcctcccaactctctctcagcccaactctctctctcaagtctgcagc	1319
Q	1893	TTTCACACCTAGACTCATGAGTGGCCAGACAAAGAGAGAGAGAGAAATAGCTCTCG	1952
D	1320	cttcaacacctagcatctcaatgagtgccaaagagagaagaagagaaatagactctgcg	1379
Q	1953	CGGTTTTTTTAAATTTGGGGGTTTTTGGCTGTTCCTTTTATGAGACCCACTTTCCTTAAT	2012
D	1380	ctgtttcttaagttctgggggtctctgcgttccctcttatagagccatctccattctctat	1439
Q	2013	AGTCAATGTTTCTTTTTCACGAGATTTATTTAGTGAAGAAACATTCATGAAATCGTACGTG	2072
D	1440	agtcacatgcttctcttctacagatatactatgaaagaacaactcacgaaatgctagctg	1499
Q	2073	CAAGTGACATCTCTTTGANTGTCAATATGGAAGATTAAACAGAGTGGAGAAATTCCTTAT	2132
D	1500	caagtgacatctctcttgatgctcatatgaaagagtctaaacacagtgaggagaatctccgat	1559
Q	2133	TCACAAATGAATGCTCTCTTTTCCCTGCCCGCCAGAACTTTTATCCACTTACCTAGATTC	2192
D	1560	tcacaatgaatagctctccctctccctcgtcccccagagccttcttaccactctccctagatct	1619

QY 2193 TACATATCTTTAAATTCATCTCAGGCCCTCCCTCAACCCAC 2235
Db 1620 tacatatctttaatttcacatcctcagccctccccaacccac 1662

RESULT 15

US-60-212-659-816
; Sequence 816, Application US/60212659
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000674
; CURRENT APPLICATION NUMBER: US/60/212,659
; CURRENT FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 879
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 816
; LENGTH: 3238
; TYPE: DNA
; ORGANISM: HUMAN
US-60-212-659-816

Query Match 44.6%; Score 1006.4; DB 46; Length 3238;
Best Local Similarity 98.9%; Pred. No. 9.3e-273;
Matches 1013; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 213 GATTTCTGGCACATCATGAGAACTGCTGACTTACATTTCTGAAAAACCATG 272
Db 1832 gatttcctggcacatcatgagaaactgctgactttacatcttcgaaacccatg 1891
QY 273 AACTGGCAAGGCGTAGAAGATTTCGCCAGACAATTAACAGATTGATGCCATACAA 332
Db 1892 aactggcaaggcgtagaagatttcgccagacaatttaacagattgattgccatacaa 1951
QY 333 AACCAAGCGGGAATTGAGTATCTGGAAGAAGCTGCGCTTCAGTCGTTCTTACTACTGG 392
Db 1952 aaccaagcggaattgagtatctggagaagactgcgcttcagtcggttcttactactgg 2011
QY 393 ATAGGAATCCGAGAGATGAGAGAAATATGACGTGGTGGAACCAACAAATCTCTCACT 452
Db 2012 ataggaatccgagagatgagagaaatatgacgtggtggaacccaacaaatctctcaact 2071
QY 453 GAAGAAGCAGAGAACTGCGGAGATGCGGAGCCCAACAAGAAAGAGAGACTGC 512
Db 2072 gaagaagcagagaaactgcggaagatgcggaagcccaacaagaaagagagactgc 2131
QY 513 GTGGAGATCTATATCAAGAGAAACAAAGATGACGCAATGGAACGATGACGCTGCCAC 572
Db 2132 gtggagatcttatatcaagagaaacaaagatgacgcaatggaaacgatatgacgctgccac 2191
QY 573 AAATTAAGCAGCGCTCTGTTACACAGCTTCTTGCCAGCCCTGCTCATGCACTGGCCAT 632
Db 2192 aaattaagcagcgctctgtttacacagcttcttgccagccctgctcatgcaactggccat 2251
QY 633 GGAGAAATGTAGAAATCAATAATCAACACTGCAACTGTGATGGGGTACTATGGG 692
Db 2252 ggagaaatgttagaaatcaataatcaaacactgcaactgtgattggggactatagg 2311
QY 693 CCCAGTGTAGCTGTGATTCAGTGTGACCTTTGGAGCCCCAGAGCTGGGTACCATG 752
Db 2312 cccagtgtagctgtgatctcagtggtgacaccttggagcccccagagctgggtaccatg 2371
QY 753 GACTGTACTCACCCCTTTGGAAACTTCAGCTTCAGCTCAGCTGAGCTGCTGCTCT 812
Db 2372 gactgtactcacccctttggaaacttcagcttcagctcagctgagctgctctc 2431
QY 813 GAAGGAACAACATTAATCTGGGATTGAGAAACACACCTGTGACCAATTGGAAATGTGCA 872
Db 2432 gaaggaacaacatctaacttggaattgagaaacacacctgtgaccaaattggaaatgtgca 2491

QY 873 TCTCCAGAACCAACCGTCAAGTGAATTCAGTGTGACCTTATATAGACACAGATTGGGG 932
Db 2492 tctccagaacccaacctgctcaagtgaatcagtgagcctctatcagaccagattgggg 2551
QY 933 ATTCAGAACTGTAGCCATCCCTGGCCAGCTTTCAGCTTACCTGCACTGATACCTTCATC 992
Db 2552 attcagaactgttagccatccctggccagcttcaagcttcaacctgcaatgaccctcatc 2611
QY 993 TGCCTAGAAGGAACAGATTAAATGGGAGAGAAACCAATTGTGATCATGTGAAATC 1052
Db 2612 tgcctagaaggaaacagattaaatgggagagaaaccaaattgtgatcatctggaatc 2671
QY 1053 TGCCTAAATCCTAGTCCATATGTCAAAAATGTGACAAAAGTTTCTCATGATTAAGGAG 1112
Db 2672 tgcctaaatcctagtcctaataatgtcaaaaatgtgacaaaagtttctcatgattaaaggag 2731
QY 1113 GGTGATTATACCCCTCTTCATTCCAGTGCAGTGCATGTTACTCATTTCTGTGGTTG 1172
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QY 1173 GCATTATATTTGGCTGCGCAGAGATTAAAAAAGGCAAGAAATCCCAAGAGAGTATG 1232
Db 2792 gcattatatttggctgcgagagattaaaaaggcaagaaatcccaagagagatg 2851
QY 1233 AATG 1236
Db 2852 aatg 2855

Search completed: January 13, 2001, 01:14:42
Job time: 16950 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2001, 16:03:50 ; Search time 1277.54 Seconds
(without alignments)
12390.935 Million cell updates/sec

Title: US-09-119-209-1
Perfect score: 2259
Sequence: 1 GAATTCACAGTCGTGGCTT.....CCGCCACACACTGGAATTC 2259

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
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 189: em_estp88:*

190: gb_gss25:*
 191: gb_gss26:*
 192: gb_gss27:*
 193: gb_gss28:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	592.8	26.2	621	97	AM950859
2	531.4	23.5	551	90	AM408490
3	504.4	22.3	632	39	AM075834
4	426.4	18.9	575	10	AA669146
5	406.4	18.0	465	143	N72396
6	403	17.8	478	20	A1434388
7	399.8	17.7	566	23	A1694304
8	388.4	17.2	459	6	AA352567
9	377.6	16.7	416	105	BE245855
10	368.6	16.3	502	91	AM474954
11	365.6	16.2	442	146	W00575
12	361	16.0	421	105	BE246681
13	360.4	16.0	505	92	AM574886
14	352.4	15.6	479	10	AA703085
15	351.8	15.6	482	39	AM083158
16	346.2	15.3	413	142	H75293
17	318	14.1	345	18	A1274577
18	315.8	14.0	483	16	A1144344
19	309.2	13.7	346	6	AA355788
20	302.4	13.4	467	38	AM015177
21	299.6	13.3	365	105	BE241595
22	299.2	13.2	435	15	A1038133
23	295.8	13.1	342	142	H70946
24	287	12.7	390	147	W85940
25	283.6	12.6	293	6	AA355761
26	283	12.5	308	139	C01368
27	279.4	12.4	419	15	A1026163
28	278.4	12.3	453	141	H00756
29	277.4	12.3	417	15	A1040572
30	274	12.1	403	21	A1540256
31	273	12.1	350	38	AV654869
32	272.4	12.1	287	145	T28911
33	271.8	12.0	411	38	AM002179
34	271.4	12.0	274	111	BE677382
35	271.4	12.0	282	6	AA361531
36	267.4	11.8	279	6	AA355982
37	267.4	11.8	396	9	AA610748
38	266.4	11.8	394	24	A1708341
39	265	11.7	297	6	AA355250
40	252.8	11.2	382	89	AM314314
41	243.4	10.8	371	22	A1572987
42	243.4	10.8	395	143	N68943
43	222	9.8	419	141	H00662
44	216.8	9.6	351	12	AA782203
45	207	9.2	599	28	A1047443

ALIGNMENTS

RESULT 1
 LOCUS AM950859
 DEFINITION EST362929 MAGE Resequences, MAGE Homo sapiens
 ACCESSION AM950859
 VERSION AM950859.1 GI:8140521
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

621 bp mRNA
 01-JUN-2000
 EST CDNA, mRNA sequence.

REFERENCE 1 (bases 1 to 621)
AUTHORS Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J., and Quackenbush, J.

TITLE Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)

COMMENT The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnd@tifg.org
Plate: 20

Seq primer: Reverse.

FEATURES
source 1. .621
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE_resequences, MAGE"
/note="Vector: pBluescriptSkm"

BASE COUNT 172 a 135 c 119 g 194 t 1 others
ORIGIN

Query Match 26.2%; Score 592.8; DB 97; Length 621;
Best Local Similarity 99.4%; Pred. No. 4.9e-157;
Matches 616; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

1210 GCAAGAAATCCAGAGAGATGATGACCCATTTAATGCCCTGGTGAAGAAAT 1269
1 GCAAGAAATCCAGAGAGATGATGACCCATTTAATGCCCTGGTGAAGAAAT 60

1270 TCTTGGAACTAAATAATCATGAGATCCTTTAAATCCTTCATGAAGCTTTGTGTG 1329
61 TCTTGGAACTAAATAATCATGAGATCCTTTAAATCCTTCATGAAGCTTTGTGTG 120

1330 GGCACCTCTACGTGAACATGAAGTGTG-TTCCTTCAGTGCATCTGGAGAACTTTTAC 1388
121 GGCACCTCTACGTGAACATGAAGTGTGTTCTTCAGTGCATCTGGAGAACTTTTAC 180

1389 CCGACCAACAGTCTCTCAGCTTCATTCGCCCCCTCATTTATCCCTCAACCCCAAGCC 1448
181 CCGACCAACAGTCTCTCAGCTTCATTCGCCCCCTCATTTATCCCTCAACCCCAAGCC 240

1449 ACAGGTGTTATACAGCTCAGCTTTTGTCTTTCTGAGGAGAAACAATAAGACAT-A 1507
241 ACAGGTGTTATACAGCTCAGCTTTTGTCTTTCTGAGGAGAAACAATAAGACATAA 300

1508 AGGGAAGATTCATGTGGAATATAAGATGGCTGACTTTGCTTTCTGACCTCTTGT 1567
301 AGGGAAGATTCATGTGGAATATAAGATGGCTGACTTTGCTTTCTGACCTCTTGT 360

1568 TTCACCTTCATTCAGTGTGCTGACTTGTGATGACAGACACTTCAATGAAGTGAATTTG 1627
361 TTCACCTTCATTCAGTGTGCTGACTTGTGATGACAGACACTTCAATGAAGTGAATTTG 420

1628 ATACATATGTAATGAGTCAAGTCTTCTGACAGATCAAAATTCAGCTGCTCTGTA 1687
421 ATACATATGTAATGAGTCAAGTCTTCTGACAGATCAAAATTCAGCTGCTCTGTA 480

1688 TACTGTGAGAGTACACTCTTATAGAAGTCAAAAAGTCTACGCTCTCTTTCTTTAA 1747
481 TACTGTGAGAGTACACTCTTATAGAAGTCAAAAAGTCTACGCTCTCTTTCTTTAA 540

1748 CTCGAGTGAAGTATGGGCTCTGCTCAAGTGAAGAGTCTATTTGACATGTAGCCTC 1807
541 CTCGAGTGAAGTATGGGCTCTGCTCAAGTGAAGAGTCTATTTGACATGTAGCCTC 600

1808 GCCGTCTGTGAATTGACCA 1827
||||||| |||||||

Db 601 GCCGTCTGTGAATTGACCA 620

RESULT 2

LOCUS AM408490 551 bp mRNA EST 16-FEB-2000
DEFINITION UI-HF-BK0-abm-g-01-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3056832 5', mRNA sequence.
AM408490
AM408490.1 GI:6927547
EST.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 551)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbdp/image/image.html
Seq primer: M13 Forward.

FEATURES
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 162 a 124 c 106 g 159 t
ORIGIN

Query Match 23.5%; Score 531.4; DB 90; Length 551;
Best Local Similarity 99.6%; Pred. No. 1.3e-139;
Matches 543; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

961 GCTTACGCTTACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
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7 GCTTACGCTTACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 66
|||||

1021 AGAAGAAAACATTTGTGAATCATCTGAATCTGCTCAATTCCTAGTCAATATGTCAAA 1080
67 AGAAGAAAACATTTGTGAATCATCTGAATCTGCTCAATTCCTAGTCAATATGTCAAA 126

1081 AATTGACAAAAGTTTCTCAATGATTAAGAGAGGATTTATTAACCCCTCTTCATTCCAG 1140
127 AATTGACAAAAGTTTCTCAATGATTAAGAGAGGATTTATTAACCCCTCTTCATTCCAG 186

1141 TGGCAGTATGTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
|||||

187 TGGCAGTATGTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 246
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1201 TAAAAAAGGCAAGAAATCAAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1260
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247 TAAAAAAGGCAAGAAATCAAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 306
|||||

OY	922	CAGTTTGGGGGATGACGAACTGTAGACCATCCCTGGCGAGCTTACGTTTACCTGTCAT	981
Db	632	CAGATTGTGGGGCTCAGC-A-AGCTGAGCCATCCCTTGGCCAGCTCAGC-TTACCTCTGGAA	575
OY	982	GTACCTTCATCTGTCTCAGAGGAACGATTAATTGGGAGGAAGAAACCTATTGTCAT	104
Db	574	TGTACCTCATCTGTCTCAGAGGAACGATTAATTGGGAGGAAGAAACCTATTGTCAT	515
OY	1042	CATCTCGAATCTGTGCAATACCTGTACCATTAATGTCAAAAATTGACAAAAGTTTCTCA	110
Db	514	CATCTCGAATCTGTGCAATACCTGTACCATTAATGTCAAAAATTGACAAAAGTTTCTCAA	455
OY	1102	TGATTAGAGAGGGGTATATTAATACCCCTCTTCAATTCAGTGCAGTCATGTTACTGCAT	1161
Db	454	TGATTAGAGAGGGGTATATTAATACCCCTCTTCAATTCAGTGCAGTCATGTTACTGCAT	395
OY	1162	TCTCTGGGTGGCATTTATCATTTTGGCTGGCAAGAGATTTAAAAAAGGCAGCAAAATTC	122

QY	1222	AGGAAAGTATAATGACCCATATTAAATGCGCTTGTTGAAGAGAAATTCCTTGCAATAC	1280
Db	334	AGAGAGATATGAT - ACCCATATTAAATTGGCTGGTGAAGAGAAATTCCTTGCAACT	276
QY	1281	TAAAAATCATAGATCTTTAAATCCTTCATGAAGCACTTTTGATGATGGCACTCTCA	1340
Db	275	TAAAAATCATAGATCTTTAAATCCTTCATGAAGCACTTTTGATGATGGCACTCTCA	216
QY	1341	CGTCAACATGAAGATGTG - TTCTTCATGAGCATCTGGGAAGATTCTACCCGACCCAAAG	1399
Db	215	CGTCAACATGAAGATGTGTTCTTCATGAGCATCTGGGAAGATTCTACCCGACCCAAAG	155

QY	1400	TTCCCTCAGCTTCGCAATTTGGCCCCCTCATTTATCCCTCAACCCCGACCCACAGGTGTTA	1459
Db	135	TTCTCTAGGCTTCGCAATTTGGCCCCCATTTATCCCTCAACCCCGACCCACAGGTGTTA	96
QY	1460	TACAGCTACGCTTTTGTCTTTCTTGAGAGAAACAATATAGCACTAAGGAAAGAT	1518
Db	95	TACAGCTACGCTTTTGTCTTTTGTGAGAGAAACAATATAGCTCATTAAGGAAAGAT	36

[illegible]

SOURCE: Human.
 ORGANISM: Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE: 1 (bases 1 to 575)
 AUTHORS: Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gelsel, G., Jost, S., J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, J., Wylie, T., Waterson, R. and Wilson, R.
 TITLE: WashU-NCI human EST project
 JOURNAL: Unpublished (1997)
 COMMENT: Washington University School of Medicine
 CONTACT: Wilson RK

Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.

Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 473.
Location/Qualifiers
1. 575

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; Site: 2: XhoI; Cloned unidirectionally. Primer: Oligo
dT, normal lung. Average insert size: 1.0 kb; Uni-ZAP XR
Vector: -5' adaptor sequence: 5' GAATTCGGCAGG 3' -3'
adaptor sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3' "

BASE COUNT 197 a 90 c 146 g 142 t

ORIGIN

Query Match 18.9% Score 426.4; DB 10; Length 575;
Best Local Similarity 98.2%; Pred. No. 8.1e-110;
Matches 442; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

QY 1786 GTCCTATTGGACATGATGACCTCCGCTGTGAATGACCATCTATTACTGCGCTC 1845
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DB 575 GTCCTATTGGACATGATGACCTCCGCTGTGAATGACCATCTATTACTGCGCTC 518
QY 1846 AGGCTCCCACTCTTTCAGCCACTCTCTTTTCAGTTGGCTGACTCCACACTAGC 1905
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DB 517 CAGCTCCCACTCTTTCAGCCACTCTCTTTTCAGTTGGCTGACTCCACACTAGC 458
QY 1906 ATCTCATGATGACCAAGCAAAAGAGAGAGAAATGACCTGGCGGGTTTCTAGTT 1965
|||||
DB 457 ATCTCATGATGACCAAGCAAAAGAGAGAGAAATGACCTGGCGGGTTTCTAGTT 398
QY 1966 TGGGGCTTTTGTCTCTTTTATGAGACCATTTCTATTCTTATAGTCAATGTTCT 2025
|||||
DB 397 TGGGGCTTTTGTCTCTTTTATGAGACCATTTCTATTCTTATAGTCAATGTTCT 338
QY 2026 TTTATTCACGATTTATTAGTAAAGAAACATCACTGAATGCTAGCTGCAAGTGCATCTC 2085
|||||
DB 337 TTTATTCACGATTTATTAGTAAAGAAACATCACTGAATGCTAGCTGCAAGTGCATCTC 278
QY 2086 TTTGATGTCATGAGAGATTTAAACAGAGGAGAAATCTTGATTCACAAATGAATG 2145
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DB 277 TTTGATGTCATGAGAGATTTAAACAGAGGAGAAATCTTGATTCACAAATGAATG 218
QY 2146 CTCTCTCTTCCCTGCCCCAGAACTTTTATCCACTTACCTAGATTCATATTCCTTTA 2205
|||||
DB 217 CTCTCTCTTCCCTGCCCCAGAACTTTTATCCACTTACCTAGATTCATATTCCTTTA 158
QY 2206 AATTTCATCTCAGGCTCTCTCAACCCAC 2235
|||||
DB 157 AATTTCATCTCAGGCTCTCTCAACCCAC 128

RESULT 5
N72396 465 bp mRNA EST 02-APR-1996
N72396
LOCUS
DEFINITION
YV39C11.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
(HUMAN); mRNA sequence.
ACCESSION
N72396
VERSION
N72396.1 GI:1229500
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 465)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,

TITLE
JOURNAL
COMMENT
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston
R., Williamson, A., Wohlmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

FEATURES
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/db_xref="taxon:9606"
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/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: p773D (Pharmacia)
with a modified polylinker; Site: 1: Pac I; Site: 2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5' AACTGGAAATTTATTTAAGATCTTTTCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Felicia Bonaldo."

BASE COUNT 123 a 107 c 103 g 127 t 5 others

ORIGIN

Query Match 18.0% Score 406.4; DB 143; Length 465;
Best Local Similarity 97.6%; Pred. No. 3.6e-104;
Matches 454; Conservative 0; Mismatches 4; Indels 7; Gaps 4;

QY 709 TGATTCAGTGTGACCTTTTGGAGCCCAAGAGCTGGGTACCATGAGCTATCACCCT 768
|||||
DB 4 TGATTCAGTGTGACCTTTTGGAGC-CCAGAGCTGGGTACCATGAGCTATCACA-CCCT 61
QY 769 TTGAAACTTCAGCTTACGCTCAGAGTGTGCTTACGCTCTGGAAGAACAACTTAA 828
|||||
DB 62 TTGAAACTTCAGCTTACA-MTCACAGTGTGCTTACGCTCTGGAAGAACAACTTAA 120
QY 829 CTGGGATTGAAGAAACCAACCGTGGACCATTTTGAACGTGTCATTCGGAACCAACCT 888
|||||
DB 121 CTGGGATTGAAGAAACCAACCGTGGACCATTTTGAACGTGTCATTCGGAACCAACCT 180
QY 889 GTCAAGTGAATTCAGTGTGACCTCTATCAGCACCAGATTTTGGGATCATGAACGTGAGC 948
|||||
DB 181 GTCAAGTGAATTCAGTGTGACCTCTATCAGCACCAGATTTTGGGATCATGAACGTGAGC 240
QY 949 ATCCCTGCGCAGCTTACGCTTACCTCTGCACTGA-CTTCACTCTCTGAGAGA 1004
|||||
DB 241 ATCCCTGCGCAGCTTACGCTTACCTCTGCACTGA-CTTCACTCTCTCTTACAGA 300
QY 1005 ACCTGAGTTAATTTGGAGAGAAACCAATTTTGAATCATCTGGAATCTGTCAAACTCT 1064
|||||
DB 301 ACCTGAGTTAATTTGGAGAGAAACCAATTTTGAATCATCTGGAATCTGTCAAACTCT 360
QY 1065 AGTCCATATGTCAAAATTTGAGCAAAAGTTTCTCAATGATTTAAGAGGCTGATTATTAAC 1124
|||||
DB 361 AGTCCATATGTCAAAATTTGAGCAAAAGTTTCTCAATGATTTAAGAGGCTGATTATTAAC 420
QY 1125 CCCCTCTTCAATTCAGTGGCAGTCAAGTGTACTGCAATTCCTGCGG 1169
|||||
DB 421 CCCCTCTTCAATTCAGTGGCAGTCAAGTGTACTGCAATTCCTGCGG 465

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FEATURES
SOURCE
    Location/Qualifiers
        1..478
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_image="2133754"
            /clone_id="NCI_CGAP_Lym12"
            /tissue_type="lymphoma, follicular mixed small and large
            /lab_host="DH10B"
            /note="Organ: lymph node; Vector: pCMV-Sport6; Site_1:
            Salt; Site_2: Notti; Cloned unidirectionally. Primer:
            Oligo dt. Average insert size 1.25 kb. Life Technologies
            catalog #: 11547-015"
150 a          90 c          98 g          139 t          1 others

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Query Match	17.86;	Score 403;	DB 20;	Length 478;
Best Local Similarity	97.18;	Pred. No.	3.3e-103;	
Matches 431; Conservative	0. w			

	AGATTAAAAAAGCGCAGAATTCACACCAAGCTT	Indels	Gaps	2;
Y	1197	II;	2;	2.

AGACATTAAAAAGCAAGATCGAAGAACTATCATTCGAGTGGCCCTT 1256

1257 GGTCGAAGAAATCTTGGAACTACTAAAAATCATGAGATCTCTTTAAATCCCTTT 385

384 GGTGAAGAAGAAATTCTTGGCAATACTAAAAATCATGAGATCCCTTTAAAATCCctmccgctcgccttc

131/ CGTTTGTGTGGCACCCTCTACGTCACACATGAGTGTG-TTCCTTACGTGCAATCTCTC 1325

524 CGTTTGTGTTGGCACCCTCTACGTCAACATGAAGTGTGTTTCNTCAGTGCATCTG 265

|||||CTTACCCGACCACAGTTCCTCAGCTTCATTTCGCCCCATTTATCCCT 1435
364 GGAACTTTTCTTTT

1436 CAACCTCCACCCGATGCTTCTTCCAGCTTCATTTCGCCCTCATTTATCCCT 205

|||||
|||GAGTGGTTCTGAGGAGAACA 1495
204 GACCCCGAGCCCTACCGCTTTTGTCTTTCTGAGGAGAACA 1495

1496 AATAGACCAT-AAGGAAACCACTTCCTC-
TTCCTTTTGTCTTTTCIGAGGAACA 145

1554

Db	144	ATAAGACCACTAAAGSGAAGGATTCATGTGGATATAAAGATGGCTGACTTGGCTTT	85
OY	1555	CTTGACCTCTGTTTTCAGTTTCAATTAGTCGTGCTCTTGATGACAGACACCTCTAAAG	161
Db	84	CTTGACCTCTGTTTTCAGTTTCAATTAGTCGTGCTCTTGATGACAGACACCTCTAAAG	25
OY	1615	AAGGCAATTTGGATACATATGTG	1638
Db	24	AAGTGCATTTTGATACATATGTG	1

RESULT	7
AI694304/c	
LOCUS	
DEFINITION	AI694304
ACCESSION	U452C04.x1 Soares.NFL.T GRC-S1 Homo sapiens cDNA clone
VERSION	AI694304
KEYWORDS	AI694304.1 GI:4971644
SOURCE	human.

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Homo sapiens					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	1 (bases 1 to 566)	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncigap .	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), unpublished (1997)	Contact: Robert C. Schreiber

JOURNAL COMMENT

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov

This clone is available royalty-free through LNLN
IMAG Consortium (Infoimage.lnl.gov) contact the
insert Length: 1429 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 458.
Location/Qualifiers
1..566
source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:231078"
/clone_id="Soares_NFL-T_GBC_S1"
/lab_host="DH10B"
/notice="Organ: pooled; Vector: pT73d-Pac (Pharmacia) with
Equal amounts of polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (Fetal lung NbHL19W, testis NTR, and B-cell
NCI-GSAP-GCB1) were mixed, and ss circles were made in
vltro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 292480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Patricia Bonaldo."
Base Count 189 a
Origin 86 c 139 g 152 t

```

Query Match	17.78;	Score 399.8;	DB 23;	Length 566;
Best Local Similarity	99.18;	Pred. No. 2.9e-102;		
Matches 423;	Conservative	0;	Mismatches	

	CGTCTGTAATGGACCATCCTAATTAACTGGCTTCAGCCGCCGC	invers	2;	Gaps	2,
1810	CGTCTGTAATGGACCATCCTAATTAACTGGCTTCAGCCGCCGC				

566 CGTCGTGATTTGGACCATCTATTACTGGCTTCA-GCCTCCCAACGCGGCGCA 1869

18/0 CCTCTCTTTTCAGTTGGCTGACTTCACACACCTAGCATCTCATGAGTGGCAACCAACG 1000

507 CCCTCTTTTTCAGTTGGCTGACTTCCACACCTAGCATCTCATGAGTCCCAAGCAAAAGC 448

1989
 TCCCTTA
 GCTTCC
 TTTGCT
 GGGGTT
 TGGGGT
 TTTAGT
 TTTTTC
 GCGGCT
 TGGCCT
 TAGCCT
 AATAGC
 GAGAGG
 GAGAGG
 1989

DB	447	ACAGAAAGAGAAATAGCGCTGGCGTGTTTT	TTAGTTGGGGGTTTTTGCCTTCTTTA	388
OY	1990	TCGAGACCAATTCCTATTTCTTATTA	TACTCAATGTTTTCTTTTATCAGCATATTA	2049
Db	387	TCGAGACCAATTCCTATTTCTTATTA	TACTCAATGTTTTCTTTTATCAGCATATTA	328
OY	2050	AAACATTCATGTAATAGCTAGCTGCAAGTAC	ATCTCTTGTGATGTCATATGNAAGTTAA	2109
Db	327	AAACATTCATGTAATAGCTAGCTGCAAGTAC	ATCTCTTGTGATGTCATATGNAAGTTAA	268
OY	2110	AAACGTCGAGAAATTCCTTGTGATTCACAT	TGAAATGCTCTCTTCCCTGCCCCAGA	2168
Db	267	AAACGTCGAGAAATTCCTTGTGATTCACAT	TGAAATGCTCTCTTCCCTGCCCCAGA	208
OY	2169	ACTTTTATTCACATTAACATGATTCACATAT	TATTTTAAATTCATTCACGAGCTCCCTCA	2228
Db	207	CTTTTATTCACATTAACATGATTCACATAT	TATTTTAAATTCATTCACGAGCTCCCTCA	148
OY	2229	ACCCGAC	2235	
Db	147	ACCCGAC	141	
RESULT	8			
AA352567		459 bp	EST	21-Apr-1997
LOCUS				
DEFINITION	AA352567	EST60518 Activated T-cells XX Homo sapiens	CDNA 5' end similar to	
ACCESSION	AA352567		selectin L, mRNA sequence.	
VERSION	AA352567.1	GI:2004887		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
	1 (bases 1 to 459)			
	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulder,R.A., Bult			
	,C.J., Lee,N.H., Kinkness,E.F., Weinstock,K.G., Gocayne,J.D., White			
	,O., Sutton,C., Blake,J.A., Brandon,R.C., Man-Whi,C., Clayton,R.A.,			
	Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald			
	,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodek,A.,			
	Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,			
	Kelley,J.C., Liu,L.-T., Marmaros,S.M., Merrick,J.T., Pelligrino,S.M.,			
	Moreno-Palacios,R.F., McDonald,L.A., Nguyen,D.T., Phillips,C.A.,			
	Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R., Small,K.V.,			
	Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Beharalik,D.P.,			
	Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dinko,D.,			
	Feng,D.-F., Fertie,A., Fischer,C., Hastings,G.A., He,M.W., Hu,J.S.,			
	Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C.,			
	HungJun,J., Li,H., Meisner,P.S., Olsen,H., Raymond,L., Wei,Y.F.,			
	Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Pannoni,M.R.,			
	Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and			
	Venter,J.C.			
TITLE	Initial assessment of human gene diversity and expression patterns			
JOURNAL	based upon 83 million nucleotides of cDNA sequence			
MEDLINE	Nature 377 (6547 suppl), 3-174 (1995)			
COMMENT	96026280			
	Other ESTs: THG172390			
	Contact: Kerlavage, AR			
	Bioinformatics			
	The Institute for Genomic Research			
	9712 Medical Center Drive, Rockville, MD 20850 USA			
	Tel: 3016699056			
	Fax: 3016699423			
	Email: arkerlavage@igrr.org			
FEATURES	For clone availability, additional sequence and expression			
	Information related to this EST, please check the TIGR Human Gene			
	Index (http://www.tigr.org/tdb/hgi/hgi.html)			
	Seq primer: M13 Reverse.			
	Location/Qualifiers			
	1..459			
	organism="Homo sapiens"			
	/db_xref="ATCC (Inhost):152766"			

BASE COUNT	137 a	93 c	91 g	132 t	6 others
ORIGIN					
Query Match	17.2%	Score 388.4	DB 6	Length 459	
Best Local Similarity	95.4%	Pred. No. 4.6e-99			
Matches 440	Conservative 0	Mismatches 16	Indels 5	Gaps 4	
OY 1000	AAGCACTGAGTAAATTGGGAAGAAACCAATTTGTGAATCAGTCGAATCTGGTCAA	1059			
DB 1	AAGCACTGAGTAAATTGGGAAGAAACCAATTTGTGAATCAGTCGAATCTGGTCAA	60			
OY 1060	ATCTGATGTCATATATGTCAAAAATTGGACAAAAGTTTCTCAATGATTAAGAGGGTGATT	1119			
DB 61	ATCTGATGTCATATATGTCAAAAATTGGACAAAAGTTTCTCAATGATTAAGAGGGTGATT	120			
OY 1120	ATAACCCCTCTTCATTCAGTGGCAAGTCATGGTATCTGATTCCTGCGGTTGCCATTTTA	1179			
DB 121	ATAACCCCTCTTCATTCAGTGGCAAGTCATGGTATCTGATTCCTGCGGTTGCCATTTTA	180			
OY 1180	TCATTTGGCTGGCAAGAGATTTAAAAAAGCAAGAAATCCAAAGCAATGATGATGACC	1239			
DB 181	TCATTTGGCTGGCAAGAGATTTAAAAAAGCAAGAAATCCAAAGCAATGATGATGACC	240			
OY 1240	CATATTAAATGCGCCCTTGGTGAAGAAAATTTCTTGGAAATCTAATAATCATGAGATCCTT	1299			
DB 241	CATATTAAATGCGCCCTTGGTGAAGAAAATTTCTTGGAAATCTAATAATCATGAGATCCTT	300			
OY 1300	TAAATCTTTCATGGAAGAGTTTGTGTGTGGTGGCAGCTCCTACGTCAACATGAGTGTG-	1358			
DB 301	TAAATCTTTCATGGAAGAGTTTGTGTGTGGTGGCAGCTCCTACGTCAACATGAGTGTG	360			
OY 1359	TTTCCTTCAGTGCATCTGGGAAGATTTCTTA-CCGAGCAACAG-TTTCCTTCAGTGCATTT	1416			
DB 361	TTTCCTTCAGTGCATCTGGGAAGATTTCTTA-CCGAGCAACAG-TTTCCTTCAGTGCATTT	420			
OY 1417	TCGCCCCCTCATTTATCCCTCAACCCCGACCGACAGGTGTT	1457			
DB 421	TTNGCCCTCATTTTTCG--TAAACCCCGACCGACAGGTGTT	459			
RESULT 9					
BE245855	416 bp	EST	13-JUL-2000		
LOCUS	TCBAP1956	pediatric pre-B cell acute lymphoblastic leukemia			
DEFINITION	Baylor-HGSC project-TCBA Homo sapiens cDNA clone TCBAP1956, mRNA				
ACCESSION	BE245855				
VERSION	BE245855.1	GI:9097603			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 416)				
JOURNAL	Wei, Y., Tsang, Y.T.M., Mel, G., Ku, J.M., Ali-Osman Jr., F.R., Muzny, D.				
COMMENT	Bouck, J., Gibbs, R.A., and Margolin, J.F.				
	pediatric leukemia cDNA sequencing project				
	unpublished (2000)				
	Contact: Dr. Judith F. Margolin				
	Human Genome Sequencing Center at Baylor College of Medicine and				
	Texas Children's Cancer Center				
	One Baylor Plaza, Houston, TX 77030, USA				
	Tel: 713 770 4536				
	Fax: 713 770 4038				
	Email: jmargin@bcmcc.org				
	Seq primer: M13 primer.				

FEATURES
SOURCE

Location/Qualifiers
1. .416
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NCBAP1956"
/clone_lib="Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project="TCBA"
/sex="male"
/tissue_type="leukopheresis"
/cell_type="pre-B cells"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
/note="Vector: lambda pSB; site_1: BamHI; site_2: EcoRI; First strand cDNA was primed with an anchored XhoI-oligo(dT) primer [5'GGAGAGCTGAGCGCGCCGAGAGAG(7)VN 3'; V-A,C,G; N=A,C,G,T] and then dg tailed. Second strand was primed with a BamHI-dC primer [5'AGGAGCTCGAGTCCGCGCCGCGCATATATATAT(C) 3']. Double-stranded cDNA was then digested with BamHI and XhoI and directionally cloned into the BamHI and SalI sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu"

BASE COUNT 123 a 87 c 110 g 95 t 1 others
ORIGIN

Query Match
Best Local Similarity 16.7%; Score 377.6; DB 105; Length 416;
Matches 402; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

QY 25 ACCTGCAGACAGACACCTCCCTT-GGCAAGAGCTGAGACCTGCTGCTAAGTCACAGA 83
DB 9 ACCTGCAGACAGACACCTCCCTTGGGCAAGAGCTGAGACCTGCTGCTAAGTCACAGA 68
QY 84 GCGTCATGGCTGCGAAGAACTAGAGAGAGCCAAAGCCATGATTTTCCATG 143
DB 69 GCGTCATGGCTGCGAAGAACTAGAGAGAGCCAAAGCCATGATTTTCCATG 128
QY 144 AATATGAGAGAGCCAGAGGACTTATGAAACATCTTCAAGTGTGGGGTGGACATG 203
DB 129 AATATGAGAGAGCCAGAGGACTTATGAAACATCTTCAAGTGTGGGGTGGACATG 188
QY 204 CTCTGTTGATTTCTGCGACATCATGACCTAGCTGCTGAGCTTCCATATTTCCATG 263
DB 189 CTCTGTTGATTTCTGCGACATCATGACCTAGCTGCTGAGCTTCCATATTTCCATG 248
QY 264 AACCCGATGAAGTGGCAAGGGCTAGAAATTTGCGGAGACATTTACAGATTTAGTT 323
DB 249 AACCCGATGAAGTGGCAAGGGCTAGAAATTTGCGGAGACATTTACAGATTTAGTT 308
QY 324 GCCATACAAAGAGGGGAATAGATCTGAGAGAGAGCTGCGCCCTTCACTGCTTCT 383
DB 309 GCCATAC-AAGCAAGGGGAATAGATCTGAGAGAGAGCTGCGCCCTTCACTGCTTCT 367
QY 384 TACTACTGATAGGAATCGGAGAGATAGAGAAATATGAGCTGGGGTGG 432
DB 368 TACTACTGATAGGAATCGGAGAGATAGAGAAATATGAGCTGGGGTGG 416

RESULT 10
AM474954/c 502 bp mRNA EST 24-FEB-2000
LOCUS hb01d12.x1 NCI-CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2881943 3',
DEFINITION AM474954 mRNA sequence.
ACCESSION AM474954
VERSION AM474954.1 GI:7045060
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 502)

AUTHORS
TITLE
JOURNAL
COMMENT

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 415.

FEATURES
SOURCE

Location/Qualifiers
1. .502
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2881943"
/clone_lib="NCI-CGAP Gas4"
/tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"
/lab_host="DH10B"
/note="Organ: stomach; Vector: pCMV-Sport6; site_1: SalI; site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"

BASE COUNT 174 a 77 c 120 g 130 t 1 others
ORIGIN

Query Match
Best Local Similarity 16.3%; Score 368.6; DB 91; Length 502;
Matches 371; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1860 TCTTCAGCCACCTCTCTTTTTCAGTTGGCTGACTTCACACCTAGCATCATGAGTCC 1919
DB 502 TCTTCAGCCACCTCTCTTTTTCAGTTGGCTGACTTCACACCTAGCATCATGAGTCC 443
QY 1920 AAGCAAGAGAGAGAGAGAAATAGCCTGCGCGTTTTCAGTTGGGGTTCCTG 1979
DB 442 AAGCAAGAGAGAGAGAGAAATAGCCTGCGCGTTTTCAGTTGGGGTTCCTG 383
QY 1980 TTTCCTTTATAGACCCATTCCTATTTCTTATAGTCAATGTTTCTTATCAGATAT 2039
DB 382 TTTCCTTTATAGACCCATTCCTATTTCTTATAGTCAATGTTTCTTATCAGATAT 323
QY 2040 ATTAGTAAGAAACATCATCTGAAATGCTAGCTGCAAGTGCATCTCTTATGTCATATG 2099
DB 322 ATTAGTAAGAAACATCATCTGAAATGCTAGCTGCAAGTGCATCTCTTATGTCATATG 263
QY 2100 GAAGAGTTAAACAGGTGAGAAATTCCTGATTCACAAATGAATGCTCCCTTCCCT 2159
DB 262 GAAGAGTTAAACAGGTGAGAAATTCCTGATTCACAAATGAATGCTCCCTTCCCT 203
QY 2160 GCCCCAGACCTTTATTCACCTTACCTAGATTTCTACATTTCTTAAATTCATCTCAG 2219
DB 202 GCCCCAGACCTTTATTCACCTTACCTAGATTTCTACATTTCTTAAATTCATCTCAG 143
QY 2220 CCTCCCTCAACCCAC 2235
DB 142 CCTCCCTCAACCCAC 127

RESULT 11
W00575 442 bp mRNA EST 15-APR-1996
LOCUS za70c12.r1 Soares_fetal_lung_NBHL19W Homo sapiens cDNA clone
DEFINITION IMAGE:297910 5' similar to PIR:S09702 S09702 leukocyte surface
protein Leu-8 precursor, short form - human ;contains element L1

repetitive element ; mRNA sequence.

ACCESSION W00575
VERSION W00575.1 GI:1272051
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 442)
Hillier, L., Clark, N., Dubuque, T., Ellison, K., Hawkins, M., Holman, M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterson, R., Williamson, A., Wohlmann, P. and Wilson, R.
The Mashu-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infoimage.llnl.gov) for further information.
Seq primer: ESTPrimer
High quality sequence stop: 367.
Location/Qualifiers
1..442
/organism="Homo sapiens"
/db_xref="GDB:1242832"
/db_xref="taxon:9606"
/clone="IMAGE:297910"
/clone_lib="Soares.fetal_lung_NbHL9W"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTACCAATCTGAGTGGGAGCGGCGCCGACATTTTGTGTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3D vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbHL9W."
BASE COUNT 121 a 94 c 81 g 143 t 3 others
ORIGIN

Query Match 16.2% Score 365.6; DB 146; Length 442;
Best Local Similarity 95.0%; Pred. No. 1.3e-92;
Matches 420; Conservative 0; Mismatches 16; Indels 6; Gaps 4;

OY 1282 AAAATCATGAGATCCCTTAATCCATGAAACGTTTGTGTCGACCTCTAC 1341
|||||
Db 1 AAAATCATGAGATCCCTTAATCCATGAAACGTTTGTGTCGACCTCTAC 60

OY 1342 GTCAACATGAGATGTG-TTCCTTCAAGTCATCTGGGAAATTTCTACCGACCAACAGT 1400
|||||
Db 61 GTCAACATGAGATGTGTTCTTCAAGTCATCTGGGAAATTTCTACCGACCAACAGT 120

OY 1401 TTCCTGAGCTTCATTTGCGCCCATTTATCCCTCAACCCCGACCGACGCTTTAT 1460
|||||
Db 121 TTCCTGAGCTTCATTTGCGCCCATTTATCCCTCAACCCCGACCGACGCTTTAT 180

OY 1461 ACACCTGAGCTTTTGTCTTTCTGAGGAGCAACAAATAGACCA-TAAGGAAAGATT 1519
|||||
Db 181 ACACCTGAGCTTTTGTCTTTCTGAGGAGCAACAAATAGACCAAGGAAAGATT 240

OY 1520 CATGTGAAATTAAGATGCGTACTTGTCTTCTTGAAGTCTTGTTCAGTTTCAT 1579
|||||
Db 241 CATGTGAAATTAAGATGCGTACTTGTCTTCTTGAAGTCTTGTTCAGTTTCAT 300

1580 TCAGTCTGTACTTGCATGACAGACACTTTCTAATGAGTGAATTTGATACATATGCA 1639
|||||
Db 301 TCAGTCTGTACTTGCATGACAGACACTTTCTAATGAGTGAATTTGATACATATGCA 360

OY 1640 ATATGAGCTCAAGTTTCTTTCAGATCAATCAATTCACGTCGCTTCTGTATACGTGAGGT 1699
|||||
Db 361 ATATGAGCTCAAG-TTTTNTTTCAGATCAATTAATTCACGTCG---TCTCTGTATCTGTGAGG 416

OY 1700 ACACCTTATAGAAAGTTCAAA 1721
|||||
Db 417 TCACCTTATAGAAAGTTCAAAA 438

RESULT 12
BE246681
LOCUS BE246681 421 bp mRNA EST 13-JUL-2000
DEFINITION TCBPAP5091 pediatric pre-B cell acute lymphoblastic leukemia
Baylor-HGSC project-TCBA Homo sapiens cDNA clone TCBPAP5091, mRNA
sequence.
ACCESSION BE246681
KEYWORDS BE246681.1 GI:9098430
EST.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 421)
Wei, Y., Tsang, Y.T.M., Mel, G., Ku, J.M., Ali-Osman, Jr., F.R., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.
Pediatric leukemia cDNA Sequencing Project
Unpublished (2000)
Contact: Dr. Judith F. Margolin
Human Genome Sequencing Center at Baylor College of Medicine and
Texas Children's Cancer Center
One Baylor Plaza, Houston, TX 77030, USA
Tel: 713 770 4536
Fax: 713 770 4038
Email: jmargin@txccc.org
Seq primer: M13 primer.
Location/Qualifiers
1..421
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TCBPAP5091"
/clone_lib="pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCBA"
/sex="male"
/tissue_type="Leukopheresis"
/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
/note="Vector: lambda PSB; Site_1: BamHI; Site_2: EcoRI;
First strand cDNA was primed with an anchored
XhoI-oligo(dT) primer [5'-GGAGGAGTCGAGCGCGCCGACGAGAG(T)VN
3'-V-A-C-G; N=A,C,G,T] and then dg tailed. Second
strand was primed with a BamHI-dc primer
[5'-AGAGGCTCGATCCGCGCGCAATATATAT(T)C 3'].
Double-stranded cDNA was then digested with BamHI and
XhoI and directionally cloned into the BamHI and XhoI
sites of lambda PSB vector. Library went through one
round of normalization. Library was constructed by Wei
Yu"

BASE COUNT 118 a 99 c 108 g 95 t 1 others
ORIGIN

Query Match 16.0% Score 361; DB 105; Length 421;
Best Local Similarity 96.8%; Pred. No. 2.6e-91;
Matches 389; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

OY 25 ACCTCACAGCAGACACTCCCTTTT-GGCAAGGAGCTGAGACCCCTTGTGCTAAGTCAAGA 83
|||||

Db 10 ACCTGCACACAGACACTCTCCCTTTGGGCAAGCACTAGAACCTTGTGTATGTCGGTA 69
 QY 84 GGCTCAATGGGCTGCAGAGAACTAGAGAGCAAGCAAGCCATGATATTCATGG 143
 Db 70 -GCTCAATGGGCTGCAGAGAACTAGAGAGCAAGCAAGCCATGATATTCATGG 128
 QY 144 AAATGTAGAGACCCAGAGGACTATGAGACATCTTCAAGTTGGGGGTGAGCAATG 203
 Db 129 AAATGTAGAGACCCAGAGGACTATGAGACATCTTCAAGTTGGGGGTGAGCAATG 188
 QY 204 CTCTGTGATATTTCCCTGGACATCATGAACTACTGCTGGAGCTTACCATTTATCTGAA 263
 Db 189 CTCTGTGATATTTCCCTGGACATCATGAACTACTGCTGGAGCTTACCATTTATCTGAA 248
 QY 264 AAACCCATGAATCGCAAAAGGCTAGAGATTTCTGCCGAGACATTTACACAGATTAGTT 323
 Db 249 AAACCCATGAATCGCAAAAGGCTAGAGATTTCTGCCGAGACATTTACACAGATTAGTT 308
 QY 324 GGCATCAAAAACAAAGCGGAAATTTGATTTCTGGAGAGACTCTGCCCTTCAGTGGTTCT 383
 Db 309 GCCATCAAAAACAAAGCGGAAATTTGATTTCTGGAGAGACTCTGCCCTTCAGTGGTTCT 368
 QY 384 TACTACTGATAGGAATCCGGAAGATAGAGGAATATGAGC 425
 Db 369 TACTACTGATAGGAATCCGGAAGATAGAGGAATATGAGC 410

RESULT 13
 AM574886 505 bp mRNA EST 15-MAR-2000
 AM574886/c UI-HF-BK0-abm-g-01-0-UI.s1 NIH_MGC_36 Homo sapiens cDNA clone
 LOCUS IMAGE:3056832 3', mRNA sequence.
 ACCESSION AM574886 GI:7246425
 VERSION AM574886
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 505)
 AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert_Strausberg@nih.gov
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/dbp/image/image.html
 Seq primer: M13 Forward
 POLVA=Yes.

FEATURES

source Location/Qualifiers
 1..505
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3056832"
 /clone_lib="NIH_MGC_36"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LT1)"
 /note="Vector: p7773-Pac Site.1: NotI; Site.2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (0.5-1.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 170 a 77 c 113 g 145 t
 ORIGIN
 Query Match 16.0%; Score 360.4; DB 92; Length 505;
 Best Local Similarity 99.7%; Pred. No. 4.2e-91;
 Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1874 TCTTTTTCAGTTGGCTGCAGCTTCCACACCTAGCATCTCATGAGTCCCAAGCAAAAGGAGAG 1933
 Db 505 TCTTTTTCAGTTGGCTGCAGCTTCCACACCTAGCATCTCATGAGTCCCAAGCAAAAGGAGAG 446
 QY 1934 AAGAGAGAAATAGGCTGCGCGGTTTTTATGTTGGGGGTTTCTGTTTCTTTTATGAG 1993
 Db 445 AAGAGAGAAATAGGCTGCGCGGTTTTTATGTTGGGGGTTTCTGTTTCTTTTATGAG 386
 QY 1994 ACCCATTCCTATTTCTTATATGATCAATGTTTCTTTATCAGATATTTATGTAAGAAAC 2053
 Db 385 ACCCATTCCTATTTCTTATATGATCAATGTTTCTTTATCAGATATTTATGTAAGAAAC 326
 QY 2054 ATCACTGAATGTAGCTGCAAGTGCATCTCTTGTATGTATGTAAGAGTTAAACA 2113
 Db 325 ATCACTGAATGTAGCTGCAAGTGCATCTCTTGTATGTATGTAAGAGTTAAACA 266
 QY 2114 GGTGAGAGAAATTCCTGTATTCACATGAATGCTCTCTTCCCTGCCCCAGAACTTT 2173
 Db 265 GTTGAGAGAAATTCCTGTATTCACATGAATGCTCTCTTCCCTGCCCCAGAACTTT 206
 QY 2174 TATCCACTTACCTAGATTTCTACATATTTCTTAATTTCAATCTCAGGCTCCCTCAACCC 2233
 Db 205 TATCCACTTACCTAGATTTCTACATATTTCTTAATTTCAATCTCAGGCTCCCTCAACCC 146
 QY 2234 AC 2235
 Db 145 AC 144

RESULT 14
 AA703085 479 bp mRNA EST 19-DEC-1997
 AA703085/c 2177g04.s1 Soares-fetal_liver_spleen_1NRLS_S1 Homo sapiens cDNA
 LOCUS IMAGE:436854 3', mRNA sequence.
 ACCESSION AA703085
 VERSION AA703085 GI:2706198
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 479)
 AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
 Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Maria,M., Martin
 'J', Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
 White,Y., Wylie,T., Waterston,R. and Wilson,R.
 WashU-NCI human EST Project
 Unpublished (1997)
 JOURNAL Contact: Wilson RK
 COMMENT Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -40m3 fwd. ET from Amersham
 High quality sequence stop: 413.

FEATURES

source Location/Qualifiers
 1..479
 /organism="Homo sapiens"
 /db_xref="GDB:1336623"
 /db_xref="taxon:9606"
 /clone="IMAGE:436854"
 /clone_lib="Soares-fetal_liver_spleen_1NRLS_S1"


```

/sex="male"
/dev-stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen INFUS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5',
AAGTGAAGATTAATTAAGATCTTTTATGAGACCATTC 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT73D vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

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BASE COUNT      163 a      77 c      111 g      128 t
ORIGIN

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Query Match      15.6%; Score 352.4; DB 10; Length 479;
Best Local Similarity 99.7%; Pred. No. 7.7e-89;
Matches 353; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1882 AGTTGGCTGACTTCACACCTAGCATCTCATGAGTGGCCAAAGAGAGAGAGA 1941
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 479 AGTTGGCTGACTTCACACCTAGCATCTCATGAGTGGCCAAAGAGAGAGA 420

QY 1942 AATAGCCCTGCGGGTTTTTGTGGGGGTTTGGCTGTTTCTTTTATGAGACCATTC 2001
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 419 AATAGCCCTGCGGGTTTTTGTGGGGGTTTGGCTGTTTCTTTTATGAGACCATTC 360

QY 2002 CTATTTCTTATAGTCAATGTTTCTTTTATGAGATATTATTAGTAAGAAACATCACTGA 2061
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 359 CTATTTCTTATAGTCAATGTTTCTTTTATGAGATATTATTAGTAAGAAACATCACTGA 300

QY 2062 AATGCTACCTGACAGTACATCTCTTTCATGATGATGAGAGATTAAGAGGTGGAGA 2121
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 299 AATGCTACCTGACAGTACATCTCTTTCATGATGATGAGAGATTAAGAGGTGGAGA 240

QY 2122 AATTCCTTGTATTCACAATGAATGCTCTCTTCCCTGCCCCCAGAACCTTTTATCCACT 2181
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 239 AATTCCTTGTATTCACAATGAATGCTCTCTTCCCTGCCCCCAGAACCTTTTATCCACT 180

QY 2182 TACCTAGATTCATACATATCTTTAAATTTTCATCTCAGGCTCCCTCAACCCAC 2235
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 179 TACCTAGATTCATACATATCTTTAAATTTTCATCTCAGGCTCCCTCAACCCAC 126

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RESULT 15
AM083158 482 bp mRNA EST 14-OCT-1999
LOCUS XG06H02.X1 NCI_CGAP_C021 Homo sapiens cDNA clone IMAGE:2583507 3',
DEFINITION mRNA sequence.
ACCESSION AM083158
VERSION AM083158.1 GI:6038310
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 482)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be

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Found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbfp/Image/Image.html
Seq primer: -400p from Gibco
High quality sequence stop: 417.
Location/Qualifiers
1..482
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2583507"
/clone_lib="NCI CGAP C021"
/tissue_type="moderately differentiated adenocarcinoma"
/lab_host="DH10B"
/note="Organ: colon; Vector: pCMV-Sport6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Normalized to Cot >500. Average insert size 1.04kb.
Normalized version of NCI-CGAP_C018. Library constructed
by Life Technologies."

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BASE COUNT      164 a      77 c      113 g      128 t
ORIGIN

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Query Match      15.6%; Score 351.8; DB 39; Length 482;
Best Local Similarity 99.4%; Pred. No. 1.1e-86;
Matches 353; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1881 CAGTTGGCTGACTTCACACCTAGCATCTCATGAGTGGCCAAAGAGAGAGAG 1940
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 482 CAGTTGGCTGACTTCACACCTAGCATCTCATGAGTGGCCAAAGAGAGAGAG 423

QY 1941 AATAGCCCTGCGGGTTTTTGTGGGGGTTTGGCTGTTTCTTTTATGAGACCATTC 2000
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 422 AATAGCCCTGCGGGTTTTTGTGGGGGTTTGGCTGTTTCTTTTATGAGACCATTC 363

QY 2001 CCTATTCTTATAGTCAATGTTTCTTTTATGAGATATTATTAGTAAGAAACATCACTG 2060
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 362 CCTATTCTTATAGTCAATGTTTCTTTTATGAGATATTATTAGTAAGAAACATCACTG 303

QY 2061 AATGCTACCTGACAGTACATCTCTTTCATGATGATGAGAGATTAAGAGGTGGAG 2120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 302 AATGCTACCTGACAGTACATCTCTTTCATGATGATGAGAGATTAAGAGGTGGAG 243

QY 2121 AATTCCTTGTATTCACAATGAATGCTCTCTTCCCTGCCCCCAGAACCTTTTATCCAC 2180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 242 AATTCCTTGTATTCACAATGAATGCTCTCTTCCCTGCCCCCAGAACCTTTTATCCAC 183

QY 2181 TTACCTAGATTCATACATATCTTTAAATTTTCATCTCAGGCTCCCTCAACCCAC 2235
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 182 TTACCTAGATTCATACATATCTTTAAATTTTCATCTCAGGCTCCCTCAACCCAC 128

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Search completed: January 12, 2001, 20:53:46
Job time: 17396 sec

```

Sat Jan 13 11:27:50 2001

us-09-119-209-1.rst

Page 12

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2001, 21:39:03 ; Search time 82.3 Seconds
(without alignments)
154.558 Million cell updates/sec

Title: US-09-119-209-2

Perfect score: 216

Sequence: 1 MIFPMKQSTQTDLMNIFKL.....WLARRLKGGKKSRSMNDPY 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_36:*

1: /cgn2_2/gcgdata/geneseq/geneseq/AA1980.DAT:*

2: /cgn2_2/gcgdata/geneseq/geneseq/AA1981.DAT:*

3: /cgn2_2/gcgdata/geneseq/geneseq/AA1982.DAT:*

4: /cgn2_2/gcgdata/geneseq/geneseq/AA1983.DAT:*

5: /cgn2_2/gcgdata/geneseq/geneseq/AA1984.DAT:*

6: /cgn2_2/gcgdata/geneseq/geneseq/AA1985.DAT:*

7: /cgn2_2/gcgdata/geneseq/geneseq/AA1986.DAT:*

8: /cgn2_2/gcgdata/geneseq/geneseq/AA1987.DAT:*

9: /cgn2_2/gcgdata/geneseq/geneseq/AA1988.DAT:*

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11: /cgn2_2/gcgdata/geneseq/geneseq/AA1990.DAT:*

12: /cgn2_2/gcgdata/geneseq/geneseq/AA1991.DAT:*

13: /cgn2_2/gcgdata/geneseq/geneseq/AA1992.DAT:*

14: /cgn2_2/gcgdata/geneseq/geneseq/AA1993.DAT:*

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20: /cgn2_2/gcgdata/geneseq/geneseq/AA1999.DAT:*

21: /cgn2_2/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2116	100.0	372	14	R37960 Human lymphocyte H
2	2116	100.0	372	14	R38908 HuLHR, Homo sapie
3	2116	100.0	372	16	R76506 Human LHR, Homo s
4	2116	100.0	372	16	R83050 Human LHR, Homo s
5	2116	100.0	372	17	R98106 Human lymphocyte c
6	2116	100.0	372	19	W37781 Homo sapiens lymph
7	2116	100.0	372	20	W73264 Human lymphocyte h
8	2110	99.7	371	17	R98122 Human lymphocyte c
9	2109	99.7	371	17	R98115 Human lymphocyte c
10	2109	99.7	371	17	R98124 Human lymphocyte c
11	2109	99.7	372	13	R24026 Sequence of human
12	2108	99.6	371	17	R98110 Human lymphocyte c

13	2108	99.6	371	17	R98113 Human lymphocyte c
14	2108	99.6	371	17	R98119 Human lymphocyte c
15	2108	99.6	372	13	R22802 Human lymphocyte h
16	2107	99.6	371	17	R98111 Human lymphocyte c
17	2107	99.6	371	17	R98112 Human lymphocyte c
18	2107	99.6	371	17	R98117 Human lymphocyte c
19	2107	99.6	371	17	R98121 Human lymphocyte c
20	2106	99.5	372	12	R12469 Human lymphocyte c
21	2105	99.5	371	17	R98116 Human lymphocyte c
22	2105	99.5	371	17	R98118 Human lymphocyte c
23	2105	99.5	371	17	R98120 Human lymphocyte c
24	2105	99.5	371	17	R98123 Human lymphocyte c
25	2104	99.4	371	17	R98109 Human lymphocyte c
26	2103	99.4	371	17	R98114 Human lymphocyte c
27	2100.5	99.3	372	17	R98133 Human lymphocyte c
28	2099.5	99.2	371	17	R98129 Human lymphocyte c
29	2099.5	99.2	374	17	R98131 Human lymphocyte c
30	2099.5	99.2	374	17	R98132 Human lymphocyte c
31	2099.5	99.2	374	17	R98134 Human lymphocyte c
32	2099.5	99.2	374	17	R98135 Human lymphocyte c
33	2096.5	99.1	370	17	R98127 Human lymphocyte c
34	2096.5	99.1	370	17	R98130 Human lymphocyte c
35	2094.5	99.0	370	17	R98126 Human lymphocyte c
36	2094.5	99.0	370	17	R98128 Human lymphocyte c
37	2090	98.8	369	17	R98125 Human lymphocyte c
38	2082	98.4	385	13	R20815 Human lymphocyte c
39	2082	98.4	385	17	R91442 Human Leu8 antigen
40	2082	98.4	385	19	W80452 Human Leu8 antigen
41	2082	98.4	385	20	W86199 Human Leu8 antigen
42	2076	98.1	385	14	R34197 Sequence encoded b
43	2076	98.1	385	15	R56653 L-selectin, Homo
44	2076	98.1	385	18	W21657 Human lymphocyte-a
45	2070	97.8	385	14	R32707 LAM-1 from PLAM-1.

ALIGNMENTS

RESULT 1	
R37960	ID
R37960 standard; Protein; 372 AA.	
XX	AC
XX	R37960;
XX	08-OCT-1993 (first entry)
DT	Human lymphocyte Homing Receptor.
XX	DE
XX	HuLHR: lymphocyte binding inhibition; lymphoma metastasis;
KW	transplant rejection; inflammation.
XX	OS
XX	Homo sapiens.
FT	Key
FT	Peptide
FT	Protein
FT	Domain
FT	Modified-site
FT	Location/Qualifiers
FT	Modified-site
FT	Modified-site
FT	Domain
FT	Modified-site
FT	Modified-site
FT	Region
FT	Modified-site
FT	Modified-site
FT	Modified-site

```

FT      Modified-site      /note="potential N-glycosylation site"
FT      246..248
FT      /note="potential N-glycosylation site"
FT      Region      259..317
FT      /label=Complement_Binding_Repeat_2
FT      Modified-site      271..273
FT      /note="potential N-glycosylation site"
FT      Modified-site      311..313
FT      /note="potential N-glycosylation site"
FT      Domain      333..355
FT      /label=Transmembrane_Domain
FT      /note="stop transfer sequence"
FT      Domain      356..372
FT      /label=Cytoplasmic_Domain
XX
XX      US5216131-A.
XX
XX      01-JUN-1993.
XX
XX      23-FEB-1989;      89US-0315015.
XX
XX      23-FEB-1989;      89US-0315015.
XX      31-OCT-1991;      91US-0786149.
XX
XX      (GETH ) GENENTECH INC.
XX
XX      Lasky LA, Rosen SD, Singer MS, Stachel SE, Yednock TA;
XX      WPI, 1993-188588/23.
XX      N-PSDB; Q43154.
XX
XX      Human and murine lymphocyte homing receptors to treat graft
XX      rejection and inflammation - comprise carbohydrate binding,
XX      epidermal growth factor and complement binding domains
XX
XX      Claim 1; Fig 1 and Fig 3; 32pp; English.
XX
XX      A human peripheral blood lymphocyte cDNA library in lambda gt10 was
XX      screened with a 2.2kb EcoRI insert of the murine Mel14 antigen clone
XX      (1.e. a murine LHR sequence). The largest EcoRI insert (2.2kb) was
XX      isolated and sequenced. The ORF codes for 372 amino acids with a mol.
XX      wt. of approximately 42,200. Comparison of the HULHR amino acid
XX      sequence with the murine LHR sequence (R37961) showed a high degree
XX      of amino acid conservation in each of the LHR domains, e.g. 96% in
XX      the transmembrane domain and 83% in the carbohydrate binding domain.
XX      The LHRs could be used to compete with the normal binding of
XX      lymphocytes to lymphoid tissue to treat inflammation or graft
XX      rejection. They could also be used to control lymphoma metastasis
XX      and to treat conditions involving lymphocyte accumulation.
XX
XX      Sequence      372 AA;
XX
Query Match      100.0%; Score 2116; DB 14; Length 372;
Best Local Similarity 100.0%; Pred. No. 3 3e-141;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      241 CGPFGNWSPEPTCOVIOCEPLSAPDGIIMNCSHPILASFSTSACTFICSGTELTCKKK 300
DB      241 CGPFGNWSPEPTCOVIOCEPLSAPDGIIMNCSHPILASFSTSACTFICSGTELTCKKK 300
QY      301 TICESSGIWNSPPIQCLDKFSFKIKEGDYNPFIPIVAVWVTFSGIAFIWLARLKK 360
DB      301 TICSSGIWNSPPIQCLDKFSFKIKEGDYNPFIPIVAVWVTFSGIAFIWLARLKK 360
QY      361 GKSKRSMDY 372
DB      361 GKSKRSMDY 372
XX
XX      RESULT      2
XX      ID      R38908 standard; Protein: 372 AA.
XX      AC      R38908;
XX      DT      11-JAN-1994 (first entry)
XX      DE      HULHR.
XX      KW      Human; murine; lymphocyte; cell surface glycoprotein; homing receptor;
XX      LHR; endothelium; lymphoid tissue; signal; domain; complement binding;
XX      carbohydrate binding; epidermal growth factor-like; egf; intracellular;
XX      transmembrane binding; cytoplasmic; ligand binding partner protein;
XX      TMD; LBPP.
XX      OS      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      FT      Peptide      20..32
XX      /note="Signal peptide"
XX      FT      Protein      39..372
XX      /note="Mature protein"
XX      FT      Domain      39..155
XX      /note="Lectin domain"
XX      FT      Domain      160..193
XX      /note="egf domain"
XX      FT      Domain      197..317
XX      /note="Complement factor binding domain"
XX      FT      Domain      333..355
XX      /note="Transmembrane binding domain"
XX      FT      Domain      356..372
XX      /note="Cytoplasmic domain"
XX
XX      US5225538-A.
XX
XX      06-JUL-1993.
XX
XX      23-FEB-1989;      89US-0315015.
XX
XX      23-FEB-1989;      89US-0315015.
XX      22-NOV-1989;      89US-0440625.
XX      16-DEC-1991;      91US-0808122.
XX
XX      (GETH ) GENENTECH INC.
XX
XX      Capon DJ, Lasky LA;
XX      WPI, 1993-226664/28.
XX      N-PSDB; Q44243.
XX
XX      New lymphocyte homing receptor immunoglobulin fusion
XX      polypeptide(s) - used to inhibit binding of lymphocytes in
XX      therapeutic and diagnostic uses
XX
XX      Disclosure; Fig 1; 44pp; English.
XX
The sequences given in R38908-09 represent human and murine lymphocyte
cell surface glycoprotein (LHR) respectively. These proteins mediate
the binding of lymphocytes to the endothelium of lymphoid tissue. LHR

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QY 241 CGPFGMWSPEPTCOVYIQCEPLSAPDLGIMNCSHPLASFSTSNCTFICSEGTLLGKK 300
 DB 241 cgpfgmwspeptcqvigceplsapdlgimncshplastsfscctficegtellgk 300
 QY 301 TICESSGIMSNPSPIQKDKSFSMIKEGYNPLFIPVAVMTAFSGLAFTIMLARLKK 360
 DB 301 ticessgimwnpspicqkdksfsmikegdympLfpvavmtafsglaftiwarlrlkk 360
 QY 361 GKSKSRMNDPY 372
 DB 361 gkkskrsmndpy 372

RESULT 4
 ID R83050 standard; Protein: 372 AA.

XX R83050;

DT 31-JAN-1996 (first entry)

XX Human LHR.

XX Lymphocyte cell surface glycoprotein; LHR; transmembrane receptor;

KW Immunoglobulin; IgG; constant region; receptor-mediated disease;

KM vector; plasma-life.

XX Homo sapiens.

XX Location/Qualifiers
 FH Key
 FT Peptide

FT /Label= Sig-peptide

FT /Label= Carbohydrate_binding_domain

FT /Label= Epidermal_growth_factor_domain

FT /Label= Complement_factor_binding_domain

FT /Label= Transmembrane_binding_domain

FT /Label= Cytoplasmic_domain

FT /note= "potential stop transfer sequence"

FT Modified-site

FT /Label= N-glycosylation_site

FT Modified-site

FT /Label= N-glycosylation_site

FT Modified-site

FT /Label= N-glycosylation_site

FT Modified-site

FT /Label= N-glycosylation_site

FT Modified-site

FT /Label= N-glycosylation_site

FT Modified-site

FT /Label= N-glycosylation_site

FT Modified-site

FT /Label= N-glycosylation_site

XX US5455165-A.

XX 03-OCT-1995.

XX 23-FEB-1989;

XX 89US-0315015.

XX 22-NOV-1989;

XX 89US-0440625.

XX 23-FEB-1989;

XX 89US-0315015.

XX 16-DEC-1991;

XX 91US-0808122.

XX 08-DEC-1992;

XX 92US-0986931.

XX 21-JAN-1994;

XX 94US-0185669.

PA (GETH) GENENTECH INC.

XX Capon DJ, Lasky LA;

XX WPI; 1995-350776/45.

XX N-PSDB; T05869.

XX Expression vector encoding fusion protein to increase plasma life -

XX comprises receptor ligand binding site and Ig constant region, for

XX treatment of receptor mediated disease

XX Dislosure; Fig 1; 42pp; English.

XX A mouse LHR (lymphocyte cell surface glycoprotein) cDNA clone was used
 to screen an oligo-dT primed lambda gt10 cDNA library derived from
 human peripheral blood lymphocyte mRNA obtd. from primary cells. A
 2.2 kb clone (sequence given in T05869) was isolated that encoded the
 human LHR protein (R83050). LHR-IgG hybrids were constructed for use in
 the targeting of therapeutic moieties to lymphoid tissue.

XX Sequence 372 AA;

Query Match 100.0%; Score 2116; DB 16; Length 372;
 Best Local Similarity 100.0%; Pred. No. 3 3e-141;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIFPMKQSTORDIMNIFKILMGWIMLCDFLAHGTVCWTHYSEKPMWQARRCRDN 60

DB 1 mlfpmkcstqrdlwnllkllgwtmlccdfiahgfcwclhysekpmmwqarrrfcdn 60

QY 61 YTDVAIQNKAIELEYLEKTLPSRSYYWIGIRKIGGIMTWGNKSLTEAENMGDGEFN 120

DB 61 ytdvalqnkaeleylektlpsrystywigirkgigwlcwgnslteeaenmgdgefn 120

QY 121 NKKNEKCEVITYIKRNKNDAGKNDACHLKAALCYTASCQWMSGHGEVEIINHTC 180

DB 121 nknkedcveiyikrnkdagkwndachlkaalcytascqwsmsgheveiinhtc 180

QY 181 NCBVGYYGPCQCVIQCEPLSAPDLGIMNCSHPLASFSTSNCTFICSEGTLLGKK 240

DB 181 ncbvgyygpcqcvigceplsapdlgimncshplastsfscctficegtellgk 240

QY 241 CGPFGMWSPEPTCOVYIQCEPLSAPDLGIMNCSHPLASFSTSNCTFICSEGTLLGKK 300

DB 241 cgpfgmwspeptcqvigceplsapdlgimncshplastsfscctficegtellgk 300

QY 301 TICESSGIMSNPSPIQKDKSFSMIKEGYNPLFIPVAVMTAFSGLAFTIMLARLKK 360

DB 301 ticessgimwnpspicqkdksfsmikegdympLfpvavmtafsglaftiwarlrlkk 360

QY 361 GKSKSRMNDPY 372

DB 361 gkkskrsmndpy 372

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

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FH Key Location/Qualifiers
FT Region 1..38
FT /label= Signal region.
FT 39..155
FT Domain /label= Lectin domain.
FT 160..193
FT Domain /label= EGF domain.
FT 197..258
FT Binding-site /label= Complement binding repeat 1.
FT 259..317
FT Binding-site /label= Complement binding repeat 2.
FT 333..355
FT Domain /label= Transmembrane domain.
FT 356..372
FT Domain /label= Cytoplasmic domain.
PN US514582-A.
PD 07-MAY-1996.
PD 23-FEB-1989; 89US-0315015.
PE 22-NOV-1989; 89US-0440625.
PR 23-FEB-1989; 89US-0315015.
PR 16-DEC-1991; 91US-0808122.
PR 08-DEC-1992; 92US-0986931.
PR 21-JAN-1994; 94US-0185670.
XX
XX (GETH ) GENENTECH INC.
XX
XX Capon DJ, Lasky LA;
XX WPI: 1996-238773/24.
XX N-PSDB: R98106.
DR
XX Nucleic acid encoding hybrid immunoglobulin comprising the ligand
PT binding site of a receptor fused to Ig constant region - useful for
PT diagnosis and treatment e.g. of inflammation
XX
XX Example 2; Figure 1: 41pp; English.
XX
XX A hybrid immunoglobulin chain comprising the ligand binding site of
CC a single transmembrane receptor without an active transmembrane
CC region; fused at its C-terminus with the N-terminus of an
CC immunoglobulin constant region. The receptor is not a member of the
CC immunoglobulin super family, nor a multiple subunit polypeptide
CC encoded by discrete genes. The hybrid immunoglobulin chain combines
CC the adhesion/targeting of a ligand binding partner (LBP) with the
CC effector functions of immunoglobulin and can bind to and/or activate
CC more than one ligand. It can be used diagnostically for the in
CC vitro assay of LBP and their targets; or therapeutically to deliver
CC LBP such as toxins, enzymes, growth factors to particular cells.
CC Typical applications are as antiviral, neuromodulating and
CC immunomodulating agents, or as modulators of cell adhesion (e.g. in
CC treating graft rejection; inflammation; metastasis etc.)
CC The immunoglobulin component increases plasma half life and
CC facilitates purification while deletion of the transmembrane region
CC potentially improves aqueous solubility and removes
CC potentially immunogenic epitopes.
XX
XX Sequence 372 AA:

```

```

Query Match 100.0%; Score 2116; DB 17; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.3e-141;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MIFPKCSTORDLWNIRKLGWTLCCDFLAHGGTYCMTYHSKPMNWRARFCRDN 60
   |||||||
Db 1 mlfpkcgstgfdlnkflkgwclmccdfiahnglycwyhsckpmnwgrarrfcfdn 60
   |||||||
QY 61 YTDLVAIQNKAIEYLYEKTLPFSSRSYVWIGIRKIGCIWTWGTNKSLEAEENMGDGEPN 120
   |||||||

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Db 61 ycdlvaigqnkaieylektlpfirsyywiglrkkgigltwvgnkslteeaenwgdgepn 120
QY 121 NKKNKEDCEIYIKRNKQAGKWNDDACHLKAALCYTASCPWSCSGHGECEITNNHTC 180
   |||||||
Db 121 nkknkedceylyikrnkdagkwndachnlkaalcyltascpwscsghgeceyllnnhtc 180
QY 181 NCDVGYGPOCLVIOCEPLAEPLGTMDCTHPFGNFSFSQCAFSQSGCTMTCIEETT* 240
   |||||||
Db 181 ncdvgygpgcqlvlyqceplaeplgltmdctthpfnfsfsqcasqsgctnltglect 240
QY 241 CGPEGNMSSPEPTCOVIOCEPLAPDLGIMNCSHPLASFSTACTFTICSEGTETIGKKK 300
   |||||||
Db 241 cgpfgnwspeptcqvlyqceplapdlgimncshplastsftactfticsegtetllykkk 300
QY 301 TICSSSGIMSNPSPICKRDKSFSMIKEGDYNPFLTPAVVMTARSGLAFTIWLARLKK 360
   |||||||
Db 301 ticsssglwsnpspicqkldksfsmkdegdnpfltpavvmtalrsglaftilwlarlkk 360
QY 361 GKSKRSMNDPY 372
   |||||||
Db 361 gkkskrsmndpy 372

RESULT 6
W37781
ID W37781 standard; Protein: 372 AA.
XX
AC W37781;
XX
DT 17-AUG-1998 (first entry)
DE Homo sapiens Lymphocyte homing receptor (LHR).
XX
XX Lymphocyte homing receptor; LHR; HuLHR; organ; graft; rejection;
KW treatment; inflammatory disorders; rheumatoid arthritis;
KW autoimmune diseases; lymphoma metastasis; control; lymphocyte;
XX accumulation.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 20..33
FT /note= "potential signal sequence"
FT 60..62
FT /note= "potential N-linked glycosylation site"
FT 104..106
FT /note= "potential N-linked glycosylation site"
FT 177..179
FT /note= "potential N-linked glycosylation site"
FT 216..218
FT /note= "potential N-linked glycosylation site"
FT 232..234
FT /note= "potential N-linked glycosylation site"
FT 246..248
FT /note= "potential N-linked glycosylation site"
FT 271..273
FT /note= "potential N-linked glycosylation site"
FT Region
FT /note= "potential N-linked glycosylation site"
FT 311..313
FT /note= "potential N-linked glycosylation site"
FT /note= "potential N-linked glycosylation site"
FT 335..357
FT /note= "membrane anchoring domain/stop transfer"
PN US5714147-A.
XX
XX
PD 03-FEB-1998.
XX
XX 23-FEB-1989; 89US-0315015.
XX 22-NOV-1989; 89US-0440625.
XX 23-FEB-1989; 89US-0315015.
XX 19-DEC-1991; 91US-0808122.
XX 08-DEC-1992; 92US-0986931.
XX 21-JAN-1994; 94US-0185670.

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PR	26-MAY-1995;	9505-0451848.
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Capon DJ, Lasky LA;	
XX		
DR	WPL: 1998-129805/12.	
XX	N-PSDB: V19012.	
PT	Prevention of lymphocyte attachment to endothelial cells - using	
PT	chimeric molecule comprising lymphocyte homing receptor and	
PT	immunoglobulin constant region	
XX		
PS	Disclosure; Fig 1: 43pp; English.	
XX		
CC	The sequence is that of a human lymphocyte homing receptor	
CC	(LHR) which may be used in the construction of a chimeric molecule	
CC	comprising an LHR fused at its C terminus to the N terminus of an	
CC	immunoglobulin constant region. This can be used for the prevention	
CC	of lymphocyte attachment to endothelial cells. Such a method may	
CC	be used for preventing organ or graft rejection, for treating	
CC	inflammatory disorders, e.g. rheumatoid arthritis or other	
CC	autoimmune diseases, for controlling lymphoma metastasis and	
CC	for treating conditions in which there is an accumulation of	
XX	lymphocytes.	
XX		
XX	Sequence 372 AA:	

Query Match	100.0%	Score 2116	DB 19	Length 372
Best Local Similarity	100.0%	Pred. No. 3,3e-141		
Matches 372	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY 1 MIPKACGQTQRLNMIFFKIMGWTLCCGFLAHHGTYCWTYIYSEKPMWQARRPCRDN 60				
Db 1 mlpwvcgstqrdlnmifkhwgmjcccdflahbglycwtlyhsekpmwqarrfcrdn 60				
QY 61 YTDVAIQKAEIEYLEKTLIPFSRSYWGIGIKGIMTWVTGNSLTFEAMNMDGEPN 120				
Db 61 ytdvaiaqkkaeileylektlpfsrsywigikgimtwvtnksltfeamnmddgepn 120				
QY 121 NKKNNEDCEIYIKRNKAKGKNDDACKRLKALCYTASCPWSCSGHGECEYIINHTC 180				
Db 121 nkknnedcevelyikrnkagkwnddackhkaalcytascpwsccsgygeceveiihnhtc 180				
QY 181 NCDVGYGPGQCLVYIQCEPLLEAPLELGTMDCTHPFCNFSFSSOCASFCSGEGNLTGIEET 240				
Db 181 ncdvgygpgqclvlyiqceplleaplelgtmdcthpfnfsfssocafcscegnltyieet 240				
QY 241 CGPFCNMSSPEPTCOYIQCEPLSAPDILINNCSPHLASFSTASCTFICSEGTLEIGKK 300				
Db 241 cgpfcnmsspeptcqvlyiqceplsapdylgimncshplasfstfaactficeqcteljqkk 300				
QY 301 TICESSGIAMSNPSPICOKLDRFSFMIRKEGQVNPLEFYAAVWYTFSGIAPLITLARLKK 360				
Db 301 ticessgjwmspspicqlkdrfsfmirkedgynplfpyavwvtafsqiaflwiarlkk 360				
QY 361 GKSKRSKSNDDPY 372				
Db 361 gkkskrsimndpy 372				

KM	lymphocyte binding; endothelium; graft rejection; inflammation; therapy
KW	arthritis; autoimmune disease; lymphoma metastasis;
XX	lymphocyte accumulation; human.
OS	Homo sapiens.
XX	
PN	US5840844-A.
XX	
XX	24-NOV-1998.
PD	
XX	
XX	10-AUG-1995; 95US-0513278.
PF	
XX	
PR	23-FEB-1989; 89US-0315015.
PR	31-OCT-1991; 91US-0786149.
PR	06-MAY-1992; 93US-0059029.
PR	10-AUG-1995; 95US-0513278.
XX	
PA	(GETH) GENENTECH INC.
PA	(REGC) UNIV CALIFORNIA.
XX	
PI	Lasky LA, Rosen SD, Singer MS, Stachel SE;
DR	WPI: 1999-034122/03.
NR	N-PSDB; V08321.

PT lymphocyte homing receptor polypeptides - useful for inhibiting
 XX lymphocyte binding to lymphoid endothelium
 PS Claim 1; Fig 1; 33pp; English.
 XX
 CC This sequence is the human lymphocyte homing receptor (LHR) of the
 CC invention. LHR is a lymphocyte cell-surface glycoprotein that mediates
 CC the binding of lymphocytes to the endothelium of lymphoid tissue. Soluble
 CC LHR polypeptides, lacking signal peptide (amino acids 1-38),
 CC transmembrane domain (amino acids 333-355) and cytoplasmic domain (amino
 CC acids 356-372), can be used therapeutically to compete with the normal
 CC binding of lymphocytes to lymphoid tissue and are especially useful for
 CC organ or graft rejection treatment protocols, and are especially useful for
 CC such as arthritis and other autoimmune diseases, for treating inflammation
 CC metastasis and for treating conditions involving lymphocyte accumulation.
 CC LHR polypeptides can also be used in assays for LHR, anti-LHR antibodies
 CC or competitive inhibitors of LHR activity, and for purifying anti-LHR
 CC antibodies, and as immunogens for raising anti-LHR antibodies.
 SQ Sequence 372 AA;

Seq	Sequence	372 AA;
QY	Query Match	100.0%; Score 2116; DB 20; Length 372;
Bst	Best Local Similarity	100.0%; Pred. No. 3.3e-141;
Matches	372; Conservative	0; Mismatches 0; Indels 0; Gaps 0
Db	1	MIFPMKQSTORDLMNIFKLMGWTMLCCDFLAHHGYCTWYHYSEKPMNMRARFCRDN 60
Db	1	mlfpmkcqstgrdmlnflkimgwtmccdfiahbgtyctwyhsckpmnmgarrifcrdn 60
QY	61	YTTDVAIQNAEIELEYEKTLPFSRSYVWYGIGKIGCITWWTGYNKSLTEBEMNGDEPN 120
Db	61	ytldvalaqlnaeleyektlpfstrsyvlgiklsglwtwgtksslteeaenmgdgnp 120
QY	121	NKKKKECEVLEYIKRNKMDAGKWNDDACHKLAALCYTSCQPMGSCGHGCEVETINNHC 180
Db	121	nkkkedcevelyikrnkmdagkwnddachklkaalcyltasqpmwscghgcevelinnhc 180
QY	181	NCDDGYGPPCCOLVIOCEPLELAEPLGTMDCHHPGNSFSSQCAFSCSESTNLGTIEET 240
Db	181	ncddgygppccqlvldceplelaeplgtmdchhpgnfsfssqcafscsestnlgtieet 240
QY	241	CGPFGMWSSEPTCOVIOCEPLSADBDGINNCSHPLASFSTSACTFICEGTELGKK 300
Db	241	cgpfgmwsseptcqlvldceplsapdldimncshplsfstsaactficegteellgk 300
QY	301	TTDESSGIMSNSPICOKLDKSFMIKRGDYNLPFVAVAVMTAFSGLAFTIILARRLK 360

D	b		301	clicssglwsmnpelcklkksfsmikegdympflfpvawvmcafsqlatilwlarrlkk	360
O	y		361	GKSKSRSMNDPY	372
D	b		361	gkkskrsmndpy	372
R	E	S	U	L	T
I	D		8		
R	9	8	122		
A	C			R98122 standard; Protein; 371 AA.	
R	9	8	122;		
D	T		01-NOV-1996	(first entry)	
X	X			Human lymphocyte cell surface glycoprotein (HULHR) variant.	
D	e				
K	M			Immunoglobulin: transmembrane receptor; adhesion; targeting;	
K	M			diagnosis; therapy; drug delivery; antiviral; neuromodulator;	
K	M			immunomodulator; cell adhesion; graft rejection; inflammation;	
X	X			metastasis.	
O	S			Homo sapiens.	
F	H			Key	
F	T			Location/Qualifiers	
F	T			1..37	
F	T			/label= Signal region.	
F	T			38..154	
F	T			/label= Lectin domain.	
F	T			159..192	
F	T			/label= EGF domain.	
F	T			196..257	
F	T			/label= Complement binding repeat 1.	
F	T			258..316	
F	T			/label= Complement binding repeat 2.	
F	T			332..354	
F	T			/label= Transmembrane domain.	
F	T			355..371	
F	T			/label= Cytoplasmic domain.	
X	X				
P	N			US5514582-A.	
P	D			07-MAY-1996.	
X	X				
P	F			23-FEB-1989;	89US-0315015.
X	X				
P	R			22-NOV-1989;	89US-0440625.
P	R			23-FEB-1989;	89US-0315015.
P	R			16-DEC-1991;	91US-0808122.
P	R			08-DEC-1992;	92US-0986931.
P	R			21-JAN-1994;	94US-0185670.
X	X				
P	A			(GETH) GENENTECH INC.	
X	X				
P	I			Capon DJ, Lasky LA;	
X	X				
D	R			WPI; 1996-238773/24.	
X	X				
P	T			Nucleic acid encoding hybrid immunoglobulin comprising the ligand	
P	T			binding site of a receptor fused to Ig constant region - useful for	
P	T			diagnosis and treatment e.g. of inflammation	
X	X				
P	S			Disclosure; Page 19; 41pp; English.	
X	X				
C	C			A hybrid immunoglobulin chain comprising the ligand binding site of	
C	C			a single transmembrane receptor without an active transmembrane	
C	C			region; fused at its C-terminus with the N-terminus of an	
C	C			immunoglobulin constant region. The receptor is not a member of the	
C	C			immunoglobulin super family, nor a multiple subunit polypeptide	
C	C			encoded by discrete genes. The hybrid immunoglobulin chain combines	
C	C			the adhesion/targeting of a ligand binding partner (LBP) with the	
C	C			effector functions of immunoglobulin and can bind to and/or activate	
C	C			more than one ligand. It can be used diagnostically for the in	

Query Match	Best Local Similarity	99.7%	Score 2110;	DB 17;	Length 371;
Matches 370;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	2	IFPMKCGSTQRDLMNIFKLMGWTMLCDFLAHHTGYCWTYHSEKPMNQARARFCRDNY	61		
DB	1	IFPMKCGSTQRDLNIFKLMGWTMLCDFLAHHTGYCWTYHSEKPMNQARARFCRDNY	60		
QY	62	TDVLAIQKAELELEYEKLPFSRSYTWGIRKIGGIMTWGVTNKSULTEDAENWGDEPN	121		
DB	61	TDVLAIQKAELELEYEKLPFSRSYTWGIRKIGGIMTWGVTNKSULTEDAENWGDEPN	120		
QY	122	KKNKEDCVIEIYIKRKKDKGKMNDDACHLKAALCYTASCPMPSCSGHCECVITNNHNCN	181		
DB	121	KKNKEDCVIEIYIKRKKDKGKMNDDACHLKAALCYTASCPMPSCSGHCECVITNNHNCN	180		
QY	182	CDVGYGFCQCLVIOCEPLAEPELTMDCITPFNGFNFSOSSCAFCSGEGTNLTGIEETTC	241		
DB	181	CDVGYGFCQCLVIOCEPLAEPELTMDCITPFNGFNFSOSSCAFCSGEGTNLTGIEETTC	240		
QY	242	GPGKMGSSPEPLCOYIOCEPLASAPDLGIMNCSHPILASFSFSACTFICSEGTELIGKKKT	301		
DB	241	GPGKMGSSPEPLCOYIOCEPLASAPDLGIMNCSHPILASFSFSACTFICSEGTELIGKKKT	300		
QY	302	ICESGIMSNSPICQKLDKSPSMKEEDDYNPLFIPVAVWYTAFCGLAFITMLARRLKKG	361		
DB	301	ICESGIMSNSPICQKLDKSPSMKEEDDYNPLFIPVAVWYTAFCGLAFITMLARRLKKG	360		
QY	362	KKSRSKMDPY 372			
DB	361	KKSRSKMDPY 371			
RESULT	9				
R98115	ID	R98115	standard; Protein; 371 AA.		
XX	AC	R98115;			
XX	DT	01-NOV-1996	(first entry)		
XX	DE	Human lymphocyte cell surface glycoprotein (HULHR) variant.			
XX	KW	Immunoglobulin; transmembrane receptor; adhesion; targeting;			
KW	KM	diagnosis; therapy; drug delivery; antiviral; neuromodulator;			
KW	KW	immunomodulator; cell adhesion; graft rejection; inflammation;			
metastasis.					
XX	OS	Homo sapiens.			
XX	Key	Location/Qualifiers			
FT	Region	1..37			
FT	Domain	/label= Signal region.			
FT	Domain	38..154			
FT	Domain	/label= Lectin domain.			
FT	Domain	159..192			
FT	Blinding-site	/label= EGF domain.			
FT	Blinding-site	196..257			

```

FT      Binding-site      /label= Complement binding repeat 1.
FT      258..316
FT      /label= Complement binding repeat 2.
FT      Domain      332..354
FT      /label= Transmembrane domain.
FT      Domain      355..371
FT      /label= Cytoplasmic domain.
PN      US5514582-A.
PD      07-MAY-1996.
XX
PF      23-FEB-1989;      89US-0315015.
PR      22-NOV-1989;      89US-0440625.
PR      23-FEB-1989;      89US-0315015.
PR      16-DEC-1991;      91US-0808122.
PR      08-DEC-1992;      92US-0986931.
PR      21-JAN-1994;      94US-0185670.
XX
PA      (GETH ) GENENTECH INC.
PI      Capon DJ, Lasky LA;
XX
DR      WPI: 1996-238773/24.
PT      Nucleic acid encoding hybrid immunoglobulin comprising the ligand
PT      binding site of a receptor fused to Ig constant region - useful for
PT      diagnosis and treatment e.g. of inflammation
XX
PS      Disclosure: Page 19; 41pp; English.
XX
CC      A hybrid immunoglobulin chain comprising the ligand binding site of
CC      a single transmembrane receptor without an active transmembrane
CC      region; fused at its C-terminus with the N-terminus of an
CC      immunoglobulin constant region. The receptor is not a member of the
CC      immunoglobulin super family, nor a multiple subunit polypeptide
CC      encoded by discrete genes. The hybrid immunoglobulin chain combines
CC      the adhesion/targetting of a ligand binding partner (LBP) with the
CC      effector functions of immunoglobulin and can bind to and/or activate
CC      more than one ligand. It can be used diagnostically for the in
CC      vitro assay of LBP and their targets; or therapeutically to deliver
CC      LBP such as toxins, enzymes, growth factors to particularly to deliver
CC      typical applications are as antiviral, neuromodulating and
CC      immunomodulating agents, or as modulators of cell adhesion (e.g. in
CC      treating graft rejection; inflammation; metastasis of lymphoma etc.)
CC      The immunoglobulin component increases plasma half life and
CC      facilitates purification while deletion of the transmembrane region
CC      facilitates recovery, improves aqueous solubility and removes
CC      potentially immunogenic epitopes. Variants of the human lymphocyte
CC      cell surface glycoprotein described in R98106 are given in
CC      R98109-R98135. This variant contains an Ile174Leu substitution.
XX
SQ      Sequence      371 AA;

```

```

Query Match      99.7%; Score 2109; DB 17; Length 371;
Best Local Similarity 99.7%; Pred. No. 1e-140;
Matches 370; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Db      |||||||
181  cdvgygypqqlvlgceplaeplgmdcthpfgnfsfscqafscsegnltglecttc 240
Qy      242  GPFGNMSPPEPTCGVIOCEPLAPDLGIMNCSHPLASPSFSACTFICSGTELIGKKT 301
Db      241  gpfgnmspeptcqvlgceplaeplgmdcthpfgnfsfscqafscsegnltglecttc 300
Qy      302  ICESGCIWSNPSPICQKLDKSFMSIRKGDYNPLFIPVAVWVTAFSGLAFIIMLARLKLK 361
Db      301  lcesgciwsnpplcqvlgceplaeplgmdcthpfgnfsfscqafscsegnltglecttc 360
Qy      362  KSKRSNMDDPY 372
Db      361  kskrsnmddpy 371

```

RESULT 10
R98124
ID R98124 standard; Protein; 371 AA.
XX
AC R98124;
XX
DT 01-NOV-1996 (first entry)
XX
DE Human lymphocyte cell surface glycoprotein (HLHR) variant.
XX
KW Immunoglobulin; transmembrane receptor; adhesion; targeting;
KW diagnosis; therapy; drug delivery; antiviral; neuromodulator;
KW immunomodulator; cell adhesion; graft rejection; inflammation;
KW metastasis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..37
FT Domain /label= Signal region.
FT Domain 38..154
FT Domain /label= Lectin domain.
FT Domain 159..192
FT Binding-site /label= EGF domain.
FT Binding-site 196..257
FT Binding-site /label= Complement binding repeat 1.
FT Binding-site 258..316
FT Domain /label= Complement binding repeat 2.
FT Domain 332..354
FT Domain /label= Transmembrane domain.
FT Domain 355..371
FT Domain /label= Cytoplasmic domain.

US5514582-A.
XX
PD 07-MAY-1996.
XX
PF 23-FEB-1989; 89US-0315015.
XX
PR 22-NOV-1989; 89US-0440625.
PR 23-FEB-1989; 89US-0315015.
PR 16-DEC-1991; 91US-0808122.
PR 08-DEC-1992; 92US-0986931.
PR 21-JAN-1994; 94US-0185670.
XX
PA (GETH) GENENTECH INC.
PI Capon DJ, Lasky LA;
XX
DR WPI: 1996-238773/24.
XX
PT Nucleic acid encoding hybrid immunoglobulin comprising the ligand
PT binding site of a receptor fused to Ig constant region - useful for
PT diagnosis and treatment e.g. of inflammation
XX
PS Disclosure: Page 19; 41pp; English.

CC A hybrid immunoglobulin chain comprising the ligand binding site of
 CC a single transmembrane receptor without an active transmembrane
 CC region; fused at its C-terminus with the N-terminus of an
 CC immunoglobulin constant region. The receptor is not a member of the
 CC immunoglobulin super family, nor a multiple subunit polypeptide
 CC encoded by discrete genes. The hybrid immunoglobulin chain combines
 CC the adhesion/targeting of a ligand binding partner (LBP) with the
 CC effector functions of immunoglobulin and can bind to and/or activate
 CC more than one ligand. It can be used diagnostically for the in
 CC vitro assay of LBP and their targets; or therapeutically to deliver
 CC LBP such as toxins, enzymes, growth factors to particular cells.
 CC Typical applications are as antiviral, neuromodulating and
 CC immunomodulating agents, or as modulators of cell adhesion (e.g. in
 CC treating graft rejection; inflammation; metastasis of lymphoma etc.)
 CC The immunoglobulin component increases plasma half life and
 CC facilitates purification while deletion of the transmembrane region
 CC facilitates recovery, improves aqueous solubility and removes
 CC potentially immunogenic epitopes. Variants of the human lymphocyte
 CC cell surface glycoprotein described in R98106 are given in
 CC R98109-R98135. This variant contains an Ile302Leu substitution.
 CC
 XX
 SO Sequence 371 AA:

Query Match 99.7%; Score 2109; DB 17; Length 371;
 Best Local Similarity 99.7%; Pred. NO. 1e-140;
 Matches 370; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPWKCGSTQRDLMNIFKLGWMTLCCDFLAHHTGYCWTYHSEKPMWQRRRCRDNY 61
 |||||||
 Db 1 ifpwkcgstqrdlmnifklgwmtlccdfilahgtycwtlyhsekpmwqrrarfcrdny 60
 |||||||
 QY 62 TDVAIQKAEIEYLEKTLFPRSRYWYIGIRKIGIMTWGKSLTEAEENMGDGEPPN 121
 |||||||
 Db 61 tdlvaigkaeieylektlfprsywyigirkigimtwgklsleaeenmgdgpenn 120
 |||||||
 QY 122 KKNKEDCEVEIYIKRNKAGKWNDDACHKLKALCYTASCPWSCSGHGCEVEIINNHTCN 181
 |||||||
 Db 121 knkedcveiyikrnkagkwnddachklkaalcytascpwsctshgceveiiinnhtcn 180
 |||||||
 QY 182 CDVGYGGQCOLVIOGELEAPELGTMDCTHPFGNFSSQCAFSCSGTINLTGEETTC 241
 |||||||
 Db 181 cdvgyggqcolviogeleapeltmdcthpfgnfssqcafscsgtintlgtgeettc 240
 |||||||
 QY 242 GPFGMSSPEPTCOYIOCEPTAPDLGIMNCSHPLASFSTACTFISSEGTETLGKKKT 301
 |||||||
 Db 241 gpfgmsspeptcoyioceptapdlgimnshplasfstsactfissegtetlgkkkt 300
 |||||||
 QY 302 ICESGIMSNPSPTICQKLDKSFSMKEGDVNPLETPVAVMTAFSGLAFTIWLARLKKG 361
 :||||||
 Db 301 icessgimsnpspticqkldksfsmkgedvnpflepavavmtafsglaftiwlarrlkkg 360
 |||||||
 QY 362 KSKRSKNDPY 372
 |||||||
 Db 361 kskrsmndpy 371

RESULT 11
 R24026
 ID R24026 standard; Protein: 372 AA.
 XX
 AC R24026;
 XX
 DT 22-NOV-1992 (first entry)
 XX
 DE Sequence of human lymphocyte cell surface glycoprotein
 XX (HLHR).
 KW Lymphocyte cell surface glycoprotein; ligand binding protein.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers

FT Peptide 1..19
 FT Peptide 20..38
 FT Modified-site /label- signal
 FT Modified-site 60..62
 FT Modified-site /label- potential N-linked glycosylation site
 FT Modified-site 104..106
 FT Modified-site /label- see above
 FT Modified-site 177..179
 FT Modified-site /label- see above
 FT Modified-site 216..218
 FT Modified-site /label- see above
 FT Modified-site 232..234
 FT Modified-site /label- see above
 FT Modified-site 271..273
 FT Modified-site /label- see above
 FT Modified-site 311..313
 FT Region /label- see above
 FT /label- stop transfer sequence
 FT /label- stop transfer sequence

US5116964-A.
 26-MAY-1992.
 22-NOV-1989; 89US-0440625.
 23-FEB-1989; 89US-0315015.
 22-NOV-1989; 89US-0440625.

(GETH) GENENTECH INC.
 Capon DJ, Lasky LA;
 WPT, 1992-199589/24.
 N-PSDB; Q24987.

Nucleic acid encoding polypeptide fusions - comprising ligand
 binding partner protein and immunoglobulin chain, for use in
 diagnosis and therapy

Disclosure: Fig 1-1 - 1-3; 43pp; English.

LHR mediates the binding of lymphocytes to the endothelium of
 lymphoid tissue. Full length cDNA clones and DNA encoding the human
 and the murine LHR (HLHR and MLHR, respectively) have been
 identified and isolated (see Q24987 and Q24988). LHR is a
 glycoprotein which contains the following protein domains: a signal
 sequence, a carbohydrate binding domain, and epidermal growth
 factor-like (egf) domain, at least one and preferably two complement
 binding domain repeat, a transmembrane binding domain (TMD), and a
 charged intracellular or cytoplasmic domain. LHR is used as the
 ligand-binding partner in fusion polypeptides with an immunoglobulin,
 for use in diagnosis and therapy.

Sequence 372 AA:

Query Match 99.7%; Score 2109; DB 13; Length 372;
 Best Local Similarity 99.7%; Pred. NO. 1e-140;
 Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIFPWKCGSTQRDLMNIFKLGWMTLCCDFLAHHTGYCWTYHSEKPMWQRRRCRDNY 60
 |||||||
 Db 1 mifpwkcgstqrdlmnifklgwmtlccdfilahgtycwtlyhsekpmwqrrarfcrdny 60
 |||||||
 QY 61 YTDVAIQKAEIEYLEKTLFPRSRYWYIGIRKIGIMTWGKSLTEAEENMGDGEPPN 120
 |||||||
 Db 61 ytdvaigkaeieylektlfprsywyigirkigimtwgklsleaeenmgdgpenn 120
 |||||||
 QY 121 KKNKEDCEVEIYIKRNKAGKWNDDACHKLKALCYTASCPWSCSGHGCEVEIINNHTC 180
 |||||||
 Db 121 knkedcveiyikrnkagkwnddachklkaalcytascpwsctshgceveiiinnhtc 180
 |||||||

```

OY 181 NCDVGYGPOCQVIOCEPLAEPELGTMDCTHPFGNFSSQCAFSQSEGNLTGIEETT 240
DB 181 ncdvgygppcqvlvqceplaepeLgtmdcthpfnfssqcafsqsegnltgieett 240
OY 241 CGPPNMSSPEPTQVIOCEPLSAPDUGIMNCSPHSFSTSACTFCSGTELGKKK 300
DB 241 cgpplgnwsspeptcqlvqceplsapdugimncshpLasfstsaactfcsgegtelgkKk 300
OY 301 TICESSGIWSNPSPICQKLDKSFMSIKEGDYNPLFIPVAVMYTAFSGLAFTIWLARRKK 360
DB 301 ticessgIwsnpSPicqkldksfmsikegdynplfipvavmytafsglafTiwlarrlKk 360
OY 361 GKSKRSNNDPY 372
DB 361 gksksrsmndpy 372

RESULT 12
R98110
ID R98110 standard; Protein; 371 AA.
XX
AC R98110;
XX
DT 01-NOV-1996 (first entry)
XX
DE Human lymphocyte cell surface glycoprotein (HuLHR) variant.
XX
KW Immunoglobulin; transmembrane receptor; adhesion; targeting;
KW diagnosis; therapy; drug delivery; antiviral; neuromodulator;
KW immunomodulator; cell adhesion; graft rejection; inflammation;
KW metastasis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..37
FT /label= Signal region.
FT Domain 38..154
FT /label= Lectin domain.
FT Domain 159..192
FT /label= EGF domain.
FT Binding-site 196..257
FT /label= Complement binding repeat 1.
FT Binding-site 258..316
FT /label= Complement binding repeat 2.
FT Domain 332..354
FT /label= Transmembrane domain.
FT Domain 355..371
FT /label= Cytoplasmic domain.
XX
PN US5514582-A.
XX
PD 07-MAY-1996.
XX
PF 23-FEB-1989; 89US-0315015.
XX
PR 22-NOV-1989; 89US-0440625.
PR 23-FEB-1989; 89US-0315015.
PR 16-DEC-1991; 91US-0808122.
PR 08-DEC-1992; 92US-0986931.
PR 21-JAN-1994; 94US-0185670.
XX
PA (GETH ) GENENTECH INC.
XX
PI Capon DJ, Lasky LA;
XX
DR WPI: 1996-238773/24.
XX
PT Nucleic acid encoding hybrid immunoglobulin comprising the ligand
PT binding site of a receptor fused to Ig constant region - useful for
PT diagnosis and treatment e.g. of inflammation
XX
PS Disclosure: Page 19; 41pp; English.

```

```

XX
CC A hybrid immunoglobulin chain comprising the ligand binding site of
CC a single transmembrane receptor without an active transmembrane
CC region; fused at its C-terminus with the N-terminus of an
CC immunoglobulin constant region. The receptor is not a member of the
CC immunoglobulin super family, nor a multiple subunit polypeptide
CC encoded by discrete genes. The hybrid immunoglobulin chain combines
CC the adhesion/targeting of a ligand binding partner (LBP) with the
CC effector functions of immunoglobulin and can bind to and/or activate
CC more than one ligand. It can be used diagnostically for the in
CC vitro assay of LBP and their targets; or therapeutically to deliver
CC LBP such as toxins, enzymes, growth factors to particularly to deliver
CC typical applications are as antiviral, neuromodulating and
CC immunomodulating agents, or as modulators of cell adhesion (e.g. in
CC treating graft rejection; inflammation; metastasis of lymphoma etc.)
CC The immunoglobulin component increases plasma half life and
CC facilitates purification while deletion of the transmembrane region
CC potentially improves aqueous solubility and removes
CC cell surface glycoprotein epitopes. Variants of the human lymphocyte
CC R98109-R98135. This variant contains an Ala71Ser substitution.
CC
SQ Sequence 371 AA:

```

```

Query Match 99.6%; Score 2108; DB 17; Length 371;
Best Local Similarity 99.7%; Pred. No. 1.2e-140;
Matches 370; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 2 IFPWKCGSTGRDLNMFEXLWGMWMLCCDFLAHNGYCTYHSEKPMWQARARECRDNY 61
DB 1 ifpwkcgstgrdlwnlflklwgmwmlccdfLahngycTyhsekpmwqararfcridny 60
OY 62 TDVIAIQNKAIELEYLEKTLPEFSRYWYIGIRKIGIMTWGYNKSLTEPARNMGDGERNN 121
DB 62 tdlvialqnkaieleylektlpEfsrywyigirkiGimtwgnkslteeparnmgdgerNN 120
OY 122 KRNKEPCVEIYIKRNKDACKWDDACHIKAAKALCYTASQCPWSCSGHCEVEIINNHTCN 181
DB 122 krnkepcveIyikrnkdackwddachikAAkAlcytasqcpwscsghceveIinnhtCN 180
OY 182 CDVGYGPOCQVIOCEPLAEPELGTMDCTHPFGNFSSQCAFSQSEGNLTGIEETT 241
DB 182 cdvgygppcqvlvqceplaepeLgtmdcthpfnfssqcafsqsegnltgieett 240
OY 242 GPPNMSSPEPTQVIOCEPLSAPDUGIMNCSPHSFSTSACTFCSGTELGKKK 301
DB 242 gppnmsspeptcqlvqceplsapdugimncshpLasfstsaactfcsgegtelgkKk 300
OY 302 TICESSGIWSNPSPICQKLDKSFMSIKEGDYNPLFIPVAVMYTAFSGLAFTIWLARRKK 361
DB 302 ticessgIwsnpSPicqkldksfmsikegdynplfipvavmytafsglafTiwlarrlKk 360
OY 362 KSKRSNNDPY 372
DB 362 kksksrsmndpy 371

RESULT 13
R98113
ID R98113 standard; Protein; 371 AA.
XX
AC R98113;
XX
DT 01-NOV-1996 (first entry)
XX
DE Human lymphocyte cell surface glycoprotein (HuLHR) variant.
XX
KW Immunoglobulin; transmembrane receptor; adhesion; targeting;
KW diagnosis; therapy; drug delivery; antiviral; neuromodulator;
KW immunomodulator; cell adhesion; graft rejection; inflammation;
KW metastasis.
XX

```

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..37
 FT Domain /label= Signal region.
 FT Domain 38..154
 FT Domain /label= Lectin domain.
 FT Domain 159..192
 FT Domain /label= EGF domain.
 FT Binding-site 196..257
 FT Binding-site /label= Complement binding repeat 1.
 FT Binding-site 258..316
 FT Binding-site /label= Complement binding repeat 2.
 FT Binding-site 332..354
 FT Domain /label= Transmembrane domain.
 FT Domain 355..371
 FT Domain /label= Cytoplasmic domain.
 XX
 PN US5514582-A.
 XX
 PD 07-MAY-1996.
 XX
 PF 23-FEB-1989; 89US-0315015.
 XX
 PR 22-NOV-1989; 89US-0440625.
 PR 23-FEB-1989; 89US-0315015.
 PR 16-DEC-1991; 91US-0808122.
 PR 08-DEC-1992; 92US-0986931.
 PR 21-JAN-1994; 94US-0185670.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Capon DJ, Lasky LA;
 XX
 DR WPI: 1996-238773/24.
 XX
 PT Nucleic acid encoding hybrid immunoglobulin comprising the ligand
 PT binding site of a receptor fused to Ig constant region - useful for
 PT diagnosis and treatment e.g. of inflammation
 XX
 PS Disclosure: Page 19; 41pp: English.
 XX
 CC A hybrid immunoglobulin chain comprising the ligand binding site of
 CC a single transmembrane receptor without an active transmembrane
 CC region: fused at its C-terminus with the N-terminus of an
 CC immunoglobulin constant region. The receptor is not a member of the
 CC immunoglobulin super family, nor a multiple subunit polypeptide
 CC encoded by discrete genes. The hybrid immunoglobulin chain combines
 CC the adhesion/targeting of a ligand binding partner (LBP) with the
 CC effector functions of immunoglobulin and can bind to and/or activate
 CC more than one ligand. It can be used diagnostically for the in
 CC vitro assay of LBP and their targets, or therapeutically to deliver
 CC LBP such as toxins, enzymes, growth factors to particular cells.
 CC Typical applications are as antiviral, neuromodulating and
 CC immunomodulating agents, or as modulators of cell adhesion (e.g. in
 CC treating graft rejection; inflammation; metastasis of lymphoma etc.)
 CC The immunoglobulin component increases plasma half life and
 CC facilitates purification while deletion of the transmembrane region
 CC facilitates recovery, improves aqueous solubility and removes
 CC potentially immunogenic epitopes. Variants of the human lymphocyte
 CC cell surface glycoprotein described in R98106 are given in
 CC R98109-R98135. This variant contains a leu150val substitution.
 XX
 SQ Sequence 371 AA;

QY 62 TDLVAIONKAELEYLEKTLPFSSRYWYIGIRKIGGIWTVGTNKSJTEBAENWGDGPNN 121
 DB 61 tdlvalgnkaeleylektlpfersywwyigirklgglwtvgtynkslteaenwgdgppn 120
 QY 122 KKNKEDCEVETIYKRNKDKAKNDACHKILKALCYTASCQPSGSGHGEVETIINNHTCN 181
 DB 121 knkedcveiytkrnkdagkwndachkvkaalcytascqpscgshgcvetlinnhtcn 180
 QY 182 CDVGYGPOCOLVIOCEPLEAPELGTMOCTHPEGNFSSQCAFSGSEGTNLGTIEHTTC 241
 DB 181 cdvgygpbqclvlgcepleapeylgtmcthpfnfssqcafscsegtnlgtieetc 240
 QY 242 GPFGNWSSPEPTQVIOCEPLSAPDLGIWNCSPHPLASFSTACPFICSEGTELIGKRT 301
 DB 241 gpfgnwsspeptcqvlgceplsapdylgimncshplasfstacpficsegtelilgkkt 300
 QY 302 ICESGSIWNSPPIQCKLDKSFMTKEGDYDPLFTPVAVMYTAFSGLAFTIWLARRLKKG 361
 DB 301 icesgsiwnspicqkldksfsmikegdydnpfltpvavmytafsglaftilwarrlkkg 360
 QY 362 KKSRSMDPY 372
 DB 361 kkskrmdpy 371
 RESULT 14
 R98119
 ID R98119 standard; Protein: 371 AA.
 XX
 AC R98119;
 XX
 DT 01-NOV-1996 (first entry)
 XX
 DE Human lymphocyte cell surface glycoprotein (HULHR) variant.
 XX
 KW Immunoglobulin: transmembrane receptor; adhesion; targeting;
 KW diagnosis; therapy; drug delivery; antiviral; neuromodulator;
 KW immunomodulator; cell adhesion; graft rejection; inflammation;
 KW metastasis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..37
 FT Domain /label= Signal region.
 FT Domain 38..154
 FT Domain /label= Lectin domain.
 FT Domain 159..192
 FT Domain /label= EGF domain.
 FT Binding-site 196..257
 FT Binding-site /label= Complement binding repeat 1.
 FT Binding-site 258..316
 FT Binding-site /label= Complement binding repeat 2.
 FT Domain 332..354
 FT Domain /label= Transmembrane domain.
 FT Domain 355..371
 FT Domain /label= Cytoplasmic domain.
 XX
 PN US5514582-A.
 XX
 PD 07-MAY-1996.
 XX
 PF 23-FEB-1989; 89US-0315015.
 XX
 PR 22-NOV-1989; 89US-0440625.
 PR 23-FEB-1989; 89US-0315015.
 PR 16-DEC-1991; 91US-0808122.
 PR 08-DEC-1992; 92US-0986931.
 PR 21-JAN-1994; 94US-0185670.
 XX
 PA (GETH) GENENTECH INC.

PI Capon DJ, Lasky LA;
 XX WPI; 1996-238773/24.
 XX
 PT Nucleic acid encoding hybrid immunoglobulin comprising the ligand
 binding site of a receptor fused to Ig constant region - useful for
 PT diagnosis and treatment e.g. of inflammation
 XX
 PS Disclosure; Page 19; 41pp; English.

XX A hybrid immunoglobulin chain comprising the ligand binding site of
 CC a single transmembrane receptor without an active transmembrane
 CC region, fused at its C-terminus with the N-terminus of an
 CC immunoglobulin constant region. The receptor is not a member of the
 CC immunoglobulin super family, nor a multiple subunit polypeptide
 CC encoded by discrete genes. The hybrid immunoglobulin chain combines
 CC the adhesion/targeting of a ligand binding partner (LBP) with the
 CC effector functions of immunoglobulin and can bind to and/or activate
 CC more than one ligand. It can be used diagnostically for the in
 CC vitro assay of LBP and their targets; or therapeutically to deliver
 CC LBP such as toxins, enzymes, growth factors to particular cells.
 CC Typical applications are as antiviral, neuromodulating and
 CC immunomodulating agents, or as modulators of cell adhesion (e.g. in
 CC treating graft rejection; inflammation; metastasis of lymphoma etc.)
 CC The immunoglobulin component increases plasma half life and
 CC facilitates recovery, improves aqueous solubility and removes
 CC potentially immunogenic epitopes. Variants of the human lymphocyte
 CC cell surface glycoprotein described in R98106 are given in
 CC R98109-R98135. This variant contains a Ser226Thr substitution.
 CC
 XX
 SQ Sequence 371 AA:

Query Match 99.6%; Score 2108; DB 17; Length 371;
 Best Local Similarity 99.7%; Pred. No. 1.2e-140;
 Matches 370; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPPMKCOSTQRIJMWIFKMGWTMLCCDFLAHGYTCWYHYSEKPMNQRARRFCRDNY 61
 DB 1 IIPWKGSTGTIDLWIFKLGWMLCCDFLAHGYTCWYHYSEKPMNQRARRFCRDNY 60
 QY 62 TDLVAIQKAEIEYEKTLPSRSRYWIGIRKIGIMTWGNTKNSITPEAENMGDEPEN 121
 DB 61 TDLVAIQKAEIEYEKTLPSRSRYWIGIRKIGIMTWGNTKNSITPEAENMGDEPEN 120
 QY 122 KKNKEDVEIYIKRNKDAKGNNDACHRLKAALCYTASCCQPMSCSGHGEVEIINHTCN 181
 DB 121 KKNKEDVEIYIKRNKDAKGNNDACHRLKAALCYTASCCQPMSCSGHGEVEIINHTCN 180
 QY 182 CDVGYGQCQCLVIGCEFLAPELGTMDCTHPGCFNSFSSQCAFSCSEGTNLGIEETTC 241
 DB 181 CDVGYGQCQCLVIGCEFLAPELGTMDCTHPGCFNSFSSQCAFSCSEGTNLGIEETTC 240
 QY 242 GPFENMWSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFTSACTFICSEGTETLIGKKT 301
 DB 241 GPFENMWSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFTSACTFICSEGTETLIGKKT 300
 QY 302 ICSSSGITMSNPICQKLDKSFMSIKEGDYNPLETIPVAVMTAFSGIAFTIMLARLKKG 361
 DB 301 ICSSSGITMSNPICQKLDKSFMSIKEGDYNPLETIPVAVMTAFSGIAFTIMLARLKKG 360
 QY 362 KKSRRSMNDPY 372
 DB 361 KKSRRSMNDPY 371

RESULT 15
 R22802
 ID R22802 standard; Protein: 372 AA.
 XX
 AC R22802;
 XX

DT 01-SEP-1992 (first entry)

XX Human lymphocyte homing receptor.

XX HuLHR; LHR; binding; endothelium; immunogens; graft; organ;
 KW rejection; inflammation; rheumatoid arthritis; lymphoma metastasis.
 XX

OS Homo sapiens.

XX Key Location/Qualifiers

XX Region

XX 20..32 /note= "potential signal sequence"

XX Modified-site /note= "N-glycosylation site"

XX Modified-site /note= "N-glycosylation site"

XX Modified-site /note= "N-glycosylation site"

XX Modified-site /note= "N-glycosylation site"

XX Modified-site /note= "N-glycosylation site"

XX Modified-site /note= "N-glycosylation site"

XX Modified-site /note= "N-glycosylation site"

XX Modified-site /note= "N-glycosylation site"

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XX Modified-site /note= "N-glycosylation site"

XX Modified-site /note= "N-glycosylation site"

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XX Modified-site /note= "N-glycosylation site"

XX Modified-site /note= "N-glycosylation site"

XX Modified-site /note= "N-glycosylation site"

XX Modified-site /note= "N-glycosylation site"

XX Modified-site /note= "N-glycosylation site"

XX Modified-site /note= "N-glycosylation site"

Query Match 99.6%; Score 2108; DB 13; Length 372;
Best Local Similarity 99.5%; Pred. No. 1.2e-140;
Matches 370; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIFPKCSTQDMLNIFKLMGWTMLCCDFLAHHGTYCTYHYSEKPMNQARRRCRDN 60
|||||
Db 1 mifpkcstqtdlwnlklwgtmlccdfiahgtycwyhysekpmnwqarrfctdn 60
61 YTDLVAIONKAEIEYLEKTLPFSSRSYWGIRKIGIMTWGNTNKSLTPEAENMGDGEPN 120
|||||
Db 61 ytdlvaionkaeieylektlpfssrswywigrlk199lwlwvgnkslpeaenwgdgepn 120
QY 121 NKKNEKDCVEIYIKRNKDAGKWNDDACHKLKAALCYTASQCPWSCSGHGECEIINNHTC 180
|||||
Db 121 nkknkqdcvealyikrnkdagkwnddachklkaalcytascqpwscsgbgeceiinnhlc 180
QY 181 NCDVGYTGPQCULVTCPELEAPELGTMDCTHPFGNFSFSQAFSCSGTNLGTGIEET 240
|||||
Db 181 ncdvgytgpqcqlvqcpeleapeltgmdcthpfgnfsfsqcafscsegtnlgtieelt 240
QY 241 CGPFGNWSPEPTCOVIOCEPLSAPDLGIMNCSHIPLASFSFTSACTFTICSEGTETLIGKK 300
|||||
Db 241 cgpfgnwspcptqv iqceplsapdlgimnchnplasfslsactflcsegtellgnkk 300
QY 301 TICSSGIMSNPSPICOKLDKSFMSIKEGDYNPLFIPIYAVWVTAFSGLAFTIWLARLKK 360
|||||
Db 301 tlcassglwnspspicqkldekelfsmklegdynplfiyavmwvtafsglafllwlarlkk 360
QY 361 GKSKSRSMNDPY 372
|||||
Db 361 gksksrsmndpy 372

Search completed: January 13, 2001, 01:15:55
Job time: 13012 sec

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Query Match 100.0%; Score 2116; DB 2; Length 372;
 Best Local Similarity 100.0%; Pred. No. 2.3e-185;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIFPMKCSOTRDLMNIFKLMGWTMLCCDPLAHHGTYCWTYHSEKPMNQRRARRCRDN 60
 Db 1 MIFPMKCSOTRDLMNIFKLMGWTMLCCDPLAHHGTYCWTYHSEKPMNQRRARRCRDN 60

QY 61 YTDVAIONKAEIYELKTLTPEFSRSYWIIGIRIGIWTWGTNKSITTEAENMGDGEFN 120
 Db 61 YTDVAIONKAEIYELKTLTPEFSRSYWIIGIRIGIWTWGTNKSITTEAENMGDGEFN 120

QY 121 NKKKEDCCEVEIYIKRNNDAGKNDACHKLKALCYTASQPMSCSGHGCEVETINNHTC 180
 Db 121 NKKKEDCCEVEIYIKRNNDAGKNDACHKLKALCYTASQPMSCSGHGCEVETINNHTC 180

QY 181 NCDVGYGPOCOLVIOCEPLAEPLGTMDCTHPFGNFSFSSQCAFSCSEGTNLGTIEETT 240
 Db 181 NCDVGYGPOCOLVIOCEPLAEPLGTMDCTHPFGNFSFSSQCAFSCSEGTNLGTIEETT 240

QY 241 CGPFGMNSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFTSACTFTCSGTELLGKKK 300
 Db 241 CGPFGMNSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFTSACTFTCSGTELLGKKK 300

QY 301 TICSSGIMNSPPTCOVIOCEPLSAPDLGIMNCSHPLASFTSACTFTCSGTELLGKKK 360
 Db 301 TICSSGIMNSPPTCOVIOCEPLSAPDLGIMNCSHPLASFTSACTFTCSGTELLGKKK 360

QY 361 GKSKSRSMNDPY 372
 Db 361 GKSKSRSMNDPY 372

RESULT 2
 5514582-2
 ; Patent No. 5514582
 ; APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A.
 ; TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
 ; IMMUNOGLOBULINS
 ; NUMBER OF SEQUENCES: 43
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/185, 670
 ; FILING DATE: 21-JAN-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 986, 931 -
 ; FILING DATE: 08-DEC-1992
 ; APPLICATION NUMBER: 808, 122
 ; FILING DATE: 16-DEC-1991
 ; APPLICATION NUMBER: 440, 625
 ; FILING DATE: 22-NOV-1989
 ; APPLICATION NUMBER: 315, 015
 ; FILING DATE: 23-FEB-1989
 ; SEQ ID NO: 2:
 ; LENGTH: 372
 5514582-2

Query Match 100.0%; Score 2116; DB 5; Length 372;
 Best Local Similarity 100.0%; Pred. No. 2.3e-185;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIFPMKCSOTRDLMNIFKLMGWTMLCCDPLAHHGTYCWTYHSEKPMNQRRARRCRDN 60
 Db 1 MIFPMKCSOTRDLMNIFKLMGWTMLCCDPLAHHGTYCWTYHSEKPMNQRRARRCRDN 60

QY 61 YTDVAIONKAEIYELKTLTPEFSRSYWIIGIRIGIWTWGTNKSITTEAENMGDGEFN 120
 Db 61 YTDVAIONKAEIYELKTLTPEFSRSYWIIGIRIGIWTWGTNKSITTEAENMGDGEFN 120

QY 121 NKKKEDCCEVEIYIKRNNDAGKNDACHKLKALCYTASQPMSCSGHGCEVETINNHTC 180
 Db 121 NKKKEDCCEVEIYIKRNNDAGKNDACHKLKALCYTASQPMSCSGHGCEVETINNHTC 180

QY 181 NCDVGYGPOCOLVIOCEPLAEPLGTMDCTHPFGNFSFSSQCAFSCSEGTNLGTIEETT 240
 Db 181 NCDVGYGPOCOLVIOCEPLAEPLGTMDCTHPFGNFSFSSQCAFSCSEGTNLGTIEETT 240

QY 241 CGPFGMNSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFTSACTFTCSGTELLGKKK 300
 Db 241 CGPFGMNSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFTSACTFTCSGTELLGKKK 300

QY 301 TICSSGIMNSPPTCOVIOCEPLSAPDLGIMNCSHPLASFTSACTFTCSGTELLGKKK 360
 Db 301 TICSSGIMNSPPTCOVIOCEPLSAPDLGIMNCSHPLASFTSACTFTCSGTELLGKKK 360

QY 361 GKSKSRSMNDPY 372
 Db 361 GKSKSRSMNDPY 372

RESULT 3
 US-08-340-539A-2
 ; Sequence 2, Application US/08340539A
 ; Patent No. 5808025
 ; GENERAL INFORMATION:
 ; APPLICANT: Tedder, Thomas F.
 ; APPLICANT: Kansas, Geoffrey S.
 ; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: FISH & NEAVE
 ; STREET: 1251 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10020
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/340,539A
 ; FILING DATE: 16-NOV-1994
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/008,459
 ; FILING DATE: 25-JAN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Gunnison, Jane
 ; REGISTRATION NUMBER: 38,479
 ; REFERENCE/DOCKET NUMBER: CG-104 CON
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-596-9000
 ; TELEFAX: 212-596-9090
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 385 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-340-539A-2

Query Match 98.1%; Score 2076; DB 1; Length 385;
 Best Local Similarity 98.1%; Pred. No. 1.1e-181;
 Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MIFPMKCSOTRDLMNIFKLMGWTMLCCDPLAHHGTYCWTYHSEKPMNQRRARRCRDN 60
 Db 14 MIFPMKCSOTRDLMNIFKLMGWTMLCCDPLAHHGTYCWTYHSEKPMNQRRARRCRDN 73

QY 61 YTDVAIONKAEIYELKTLTPEFSRSYWIIGIRIGIWTWGTNKSITTEAENMGDGEFN 120
 Db 61 YTDVAIONKAEIYELKTLTPEFSRSYWIIGIRIGIWTWGTNKSITTEAENMGDGEFN 120

Db 74 YTDVAIONKAEIELEKTLFSPRSYWIIGIRKIGIWTWGTNKSLEEAENMDGEPN 133
QY 121 NKKNKEDCEVEIYIKRNKDGAKMNDACHKLAALCYTASCPWSCSGHGECEVEIINNHTC 180
Db 134 NKKNKEDCEVEIYIKRNKDGAKMNDACHKLAALCYTASCPWSCSGHGECEVEIINNHTC 193
QY 181 NCDVGYGPOQVYIQCEPLAPELGTMDCTHPGNFSSQCAFSCSEGTNLGIEETT 240
Db 194 NCDVGYGPOQVYIQCEPLAPELGTMDCTHPGNFSSQCAFSCSEGTNLGIEETT 253
QY 241 CGPFGNMSPEPTCOVIOCEPLSAPDLGIMNC SHPLASFSTSACTFICSEGTTELIGKK 300
Db 254 CEPFGNMSPEPTCOVIOCEPLSAPDLGIMNC SHPLASFSTSACTFICSEGTTELIGKK 313
QY 301 TICSSGIMSNPSPIQKLDKFSMKEGDYNPLFIPAAVWVTAFFSGLAFIIMLARLKK 360
Db 314 TICSSGIMSNPSPIQKLDKFSMKEGDYNPLFIPAAVWVTAFFSGLAFIIMLARLKK 373
QY 361 GKSKRSMDPY 372
Db 374 GKSKRSMDPY 385

RESULT 4
US-08-461-592B-2
; Sequence 2, Application US/08461592B
; Patent No. 5834425
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; APPLICANT: Kansas, Geoffrey S.
; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
; TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,592B
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/340,539
; FILING DATE: 16-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,459
; FILING DATE: 25-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: CG-104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-461-592B-2

Query Match 98.1%; Score 2076; DB 2; Length 385;

Best Local similarity 98.1%; Pred. No. 1,1e-181;
Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 MIFPWKCOSTQORDLWNTKRLMGWTLCCDFLAHSTYCWTHYSEKPMNQARARFCNDN 60
Db 14 MIFPWKCOSTQORDLWNTKRLMGWTLCCDFLAHSTYCWTHYSEKPMNQARARFCNDN 73
QY 61 YTDVAIONKAEIELEKTLFSPRSYWIIGIRKIGIWTWGTNKSLEEAENMDGEPN 120
Db 74 YTDVAIONKAEIELEKTLFSPRSYWIIGIRKIGIWTWGTNKSLEEAENMDGEPN 133
QY 121 NKKNKEDCEVEIYIKRNKDGAKMNDACHKLAALCYTASCPWSCSGHGECEVEIINNHTC 180
Db 134 NKKNKEDCEVEIYIKRNKDGAKMNDACHKLAALCYTASCPWSCSGHGECEVEIINNHTC 193
QY 181 NCDVGYGPOQVYIQCEPLAPELGTMDCTHPGNFSSQCAFSCSEGTNLGIEETT 240
Db 194 NCDVGYGPOQVYIQCEPLAPELGTMDCTHPGNFSSQCAFSCSEGTNLGIEETT 253
QY 241 CGPFGNMSPEPTCOVIOCEPLSAPDLGIMNC SHPLASFSTSACTFICSEGTTELIGKK 300
Db 254 CEPFGNMSPEPTCOVIOCEPLSAPDLGIMNC SHPLASFSTSACTFICSEGTTELIGKK 313
QY 301 TICSSGIMSNPSPIQKLDKFSMKEGDYNPLFIPAAVWVTAFFSGLAFIIMLARLKK 360
Db 314 TICSSGIMSNPSPIQKLDKFSMKEGDYNPLFIPAAVWVTAFFSGLAFIIMLARLKK 373
QY 361 GKSKRSMDPY 372
Db 374 GKSKRSMDPY 385

RESULT 5
US-08-513-278-4
; Sequence 4, Application US/08513278
; Patent No. 5840844
; GENERAL INFORMATION:
; APPLICANT: LASKY, LAURENCE A.
; APPLICANT: STACHELL, SCOTT E.
; APPLICANT: ROSEN, STEVEN D.
; APPLICANT: SINGER, MARK S.
; APPLICANT: YEDNICK, TED A.
; TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,278
; FILING DATE: 10-AUG-1995
; CLASSIFICATION: 5530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/059027
; FILING DATE: 06-MAY-1993
; APPLICATION NUMBER: 07/786149
; FILING DATE: 31-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/315015
; FILING DATE: 23-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 565D1C1
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-513-278-4

Query Match
Best Local Similarity 76.1%; Score 1651; DB 2; Length 372;
Matches 283; Conservative 32; Mismatches 57; Indels 0; Gaps 0;

QY 1 MIFPMKQSTQRLDNIETKLMGWTMLCCDFLAHNGTCTYHYSEKPMNMRARFCRDN 60
DB 1 MIFPMKQSTQRLDNIETKLMGWTMLCCDFLAHNGTCTYHYSEKPMNMRARFCRDN 60
QY 61 YTDVAIONKKAIEYLENTLPKSPSYWIGIRKIGKMTWVGTNKTJTEAENMGAGEPN 120
DB 61 YTDVAIONKKAIEYLENTLPKSPSYWIGIRKIGKMTWVGTNKTJTEAENMGAGEPN 120
QY 121 NKKNKEDCEVEIYIKRERDSGKMNDDACHKRAALCTYASQPSGSCGHCVEIINNHTC 180
DB 121 NKKNKEDCEVEIYIKRERDSGKMNDDACHKRAALCTYASQPSGSCGHCVEIINNHTC 180
QY 181 NCDVGYGQCVLYIOCEPLAPELGTMDCHPFGNFSFSCAFSCSEGTNLGTIEET 240
DB 181 NCDVGYGQCVLYIOCEPLAPELGTMDCHPFGNFSFSCAFSCSEGTNLGTIEET 240
QY 241 CGPFGNWSPEPTQVIOCEPLAPDLGIMNCSHPLASFSFTSACTFICSEGTILGKK 300
DB 241 CGPFGNWSPEPTQVIOCEPLAPDLGIMNCSHPLASFSFTSACTFICSEGTILGKK 300
QY 301 TICSSGSIWNSPICOQKLOKSFMSIKEGDYNPFIPIVAVMTAFSGLAFTIWLARLKK 360
DB 301 TICSSGSIWNSPICOQKLOKSFMSIKEGDYNPFIPIVAVMTAFSGLAFTIWLARLKK 360
QY 361 GKSKRSMDPY 372
DB 361 GKSKRSMDPY 372

RESULT 6
5514582-4
PATENT NO. 5514582
APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A.
TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
IMMUNOLOGICALS
NUMBER OF SEQUENCES: 43
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,670
FILING DATE: 21-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 986,931
FILING DATE: 08-DEC-1992
APPLICATION NUMBER: 808,122
FILING DATE: 16-DEC-1991
APPLICATION NUMBER: 440,625
FILING DATE: 22-NOV-1989
APPLICATION NUMBER: 315,015
FILING DATE: 23-FEB-1989
SEQ ID NO: 4
LENGTH: 372
5514582-4

Query Match
Best Local Similarity 76.1%; Score 1651; DB 5; Length 372;
Matches 283; Conservative 32; Mismatches 57; Indels 0; Gaps 0;
QY 1 MIFPMKQSTQRLDNIETKLMGWTMLCCDFLAHNGTCTYHYSEKPMNMRARFCRDN 60

DB 1 MIFPMKQSTQRLDNIETKLMGWTMLCCDFLAHNGTCTYHYSEKPMNMRARFCRDN 60
QY 61 YTDVAIONKKAIEYLENTLPKSPSYWIGIRKIGKMTWVGTNKTJTEAENMGAGEPN 120
DB 61 YTDVAIONKKAIEYLENTLPKSPSYWIGIRKIGKMTWVGTNKTJTEAENMGAGEPN 120
QY 121 NKKNKEDCEVEIYIKRERDSGKMNDDACHKRAALCTYASQPSGSCGHCVEIINNHTC 180
DB 121 NKKNKEDCEVEIYIKRERDSGKMNDDACHKRAALCTYASQPSGSCGHCVEIINNHTC 180
QY 181 NCDVGYGQCVLYIOCEPLAPELGTMDCHPFGNFSFSCAFSCSEGTNLGTIEET 240
DB 181 NCDVGYGQCVLYIOCEPLAPELGTMDCHPFGNFSFSCAFSCSEGTNLGTIEET 240
QY 241 CGPFGNWSPEPTQVIOCEPLAPDLGIMNCSHPLASFSFTSACTFICSEGTILGKK 300
DB 241 CGPFGNWSPEPTQVIOCEPLAPDLGIMNCSHPLASFSFTSACTFICSEGTILGKK 300
QY 301 TICSSGSIWNSPICOQKLOKSFMSIKEGDYNPFIPIVAVMTAFSGLAFTIWLARLKK 360
DB 301 TICSSGSIWNSPICOQKLOKSFMSIKEGDYNPFIPIVAVMTAFSGLAFTIWLARLKK 360
QY 361 GKSKRSMDPY 372
DB 361 GKSKRSMDPY 372

RESULT 7
US-08-110-158-4
Sequence 4, Application US/08110158
Patent No. 5605821
GENERAL INFORMATION:
APPLICANT: McEver, Rodger P.
APPLICANT: Pan, Junliang
TITLE OF INVENTION: Expression Control Sequences of the
TITLE OF INVENTION: P-Selectin Gene
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,158
FILING DATE: 19930820
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/320,408
FILING DATE: 08-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-815-6558
TELEFAX: (404)-815-6555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 830 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-110-158-4


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? OTHER INFORMATION: glycosylation site"
?
? FEATURE:
? NAME/KEY: Binding-site
? LOCATION: 665
? OTHER INFORMATION: /note= "Potential asparagine-linked
? OTHER INFORMATION: glycosylation site"
?
? FEATURE:
? NAME/KEY: Binding-site
? LOCATION: 716
? OTHER INFORMATION: /note= "Potential asparagine-linked
? OTHER INFORMATION: glycosylation site"
?
? FEATURE:

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[illegible]

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RESULT 9
5378464-2
; Patent No. 5378464
; APPLICANT: MCEIVER, RODGER P.
; TITLE OF INVENTION: MODULATION OF INFLAMMATORY RESPONSES
; BY ADMINISTRATION OF GMP-140 OR ANTIBODY TO GMP-140
; NUMBER OF SEQUENCES: 32
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/320,408
; FILING DATE: 08-MAR-1989
; SEQ ID NO:2:
; LENGTH: 830
5378464-2

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Query Match 42.0%; Score 889; DB 5; Length 830;
Best Local Similarity 50.0%; Pred. No. 6.1e-73;
Matches 155; Conservative 48; Mismatches 107; Indels 0; Gaps 0;

[illegible]


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Best Local Similarity   36.1%; Pred. No. 1,9e-66;
Matches 159; Conservative 55; Mismatches 109; Indels 117; Gaps 7;

Oy      39 WTHYHSKPPNNMQRARFCRDNTDVLAIQNKAEIIELEKTLPSRSRYWIGIRRGISW 98
       ||| | : : : : : ||| | : : : : : ||| | : : : : : ||| | : : : : :
Db      23 WSYSASTETITFEDDAAYCOQRYTHLVAIONHAEILEYLNSTFNYSASYWIGIRKINGT 82
Oy      99 TWGTNKSSTEEAENMGDEPNPKKKREDCVEITYIKRNKDAGKNDDACHKLAKALCYTA 158
       ||| | : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
Db      83 TWIGTKKALLPRTTNAPREPNNKSNEDCVETIYIKRDKDSKMKNDKESKKKIALCYTA 142
Oy      159 SCOPMSCSGHGECVELIINNHTCNCVDVGYGQCQOLVIOCEPLAEPLGTMDCT----- 211
       ||| | : : : : : ||| | : : : : : ||| | : : : : : ||| | : : : : :
Db      143 ACPHTSCGHGEICETINSTCQCYPFERGLCEQVEVEDADLENVNVCVPQSLPWMT 202
Oy      212 -----HP-----PGNFS 218
       ||| | : : : : : ||| | : : : : : ||| | : : : : : ||| | : : : : :
Db      203 TCFAFECKBEFLIGEPEHLQCTSSGSMDGKKPRCAVTCDTVGHQNQDNVSCNHSSIFE 262
Oy      219 FSSQACFCSGESTNLTGIEETCGPFGNMSSBEPYCQVIOCEPLSAPDLGIMNSCH-PLA 277
       ||| | : : : : : ||| | : : : : : ||| | : : : : : ||| | : : : : :
Db      263 YKSTCHFTCAEGFGLQGPAQIRCTAQOGMTQDAPACKAVKCPAAVSOPRNGLVKRTHTSPTG 322
Oy      278 SRSPTSACFFLTSETELLGKKKTICESSGGTWSNPSPICQ-----KLDKSFSMIREGD 330
       ||| | : : : : : ||| | : : : : : ||| | : : : : : ||| | : : : : :
Db      323 ETTYSSCAFSCBEBEELRGAHQLAQTSGQGWTOGEVPCQYVQCSSLEVPREIMSCSGE 382
Oy      331 VNPILF-----IPVAVMVTA---- 344
       ||| | : : : : : ||| | : : : : : ||| | : : : : : ||| | : : : : :
Db      383 --PVFGAVCTFACPFGMWLNQSVALTGCATGHWMSGMLPTCEAPAESHKIPLAMGLAAGVS 440
Oy      345 -FSGSLAFIVWLARRLKRRKK 363
       ||| | : : : : : ||| | : : : : : ||| | : : : : : ||| | : : : : :
Db      441 FWTSASFLLMLRLKRKRK 460

RESULT 14
US-09-276-197-9
: Sequence 9, Application US/09276197
: Patent No. 6040428
: GENERAL INFORMATION:
: APPLICANT: Rollins, Scott
: APPLICANT: Rother, Russell P.
: APPLICANT: Evans, Mark J.
: APPLICANT: Mattis, Louis A.
: TITLE OF INVENTION: PORCINE E-SELECTIN
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Seth A. Fidel
: STREET: 25 Science Park, Box 15
: CITY: New Haven
: STATE: Connecticut
: COUNTRY: USA
: ZIP: 06511
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 750 Kb storage
: OPERATING SYSTEM: DOS 6.2
: SOFTWARE: Wordperfect 6.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/276,197
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/252,493
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Fidel, Seth A.
: REGISTRATION NUMBER: 38,449
: REFERENCE/DOCKET NUMBER: ALX-138
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (203) 776-1790
: TELEFAX: (203) 772-3655

```

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OM protein - protein search, using sw model

Run on: January 13, 2001, 00:37:13 : Search time 127.23 Seconds
(without alignments)
427.383 Million cell updates/sec

Title: US-09-119-209-2

Perfect score: 2116
Sequence: 1 MIFPMKOSTORDLMNIFKL.....WLARLKGKSKSRMNDPY 372

Scoring table: HLOSUM62
Capop 10.0 , Capext 0.5

Searched: 901307 seqs, 146172015 residues

Total number of hits satisfying chosen parameters: 901307

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA:*
1: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
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25: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
26: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
27: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*
28: /cgn2_6/ptodata/2/paa/US086_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2116	100.0	372	15	US-09-119-209-2
2	2076	98.1	385	1	PCT-US92-03970-2
3	2076	98.1	385	1	PCT-US94-00909-2
4	2076	98.1	385	4	US-08-008-459-2
5	2076	98.1	385	7	US-08-340-539-2

6	2076	98.1	385	8	US-08-410-569-2
7	1883	89.0	1078	22	US-60-212-659-523
8	1879	88.8	1078	22	US-60-207-315-428
9	1879	88.8	1078	22	US-60-230-435-1751
10	1651	78.0	372	15	US-09-119-209-4
11	905	42.8	830	1	PCT-US94-09395-4
12	905	42.8	830	1	US-08-449-687B-4
13	905	42.8	830	1	US-08-449-687B-4
14	862	40.7	610	22	US-60-207-315-467
15	862	40.7	610	10	PCT-US99-28965-19
16	862	40.7	610	11	US-08-657-753-2
17	862	40.7	610	11	US-08-770-435-3
18	666	31.5	119	22	US-09-009-490A-89
19	666	31.5	119	22	US-60-160-189-8687
20	645	30.5	119	22	US-60-169-867-5823
21	645	30.5	119	22	US-60-160-203-5003
22	586	27.7	116	22	US-60-169-840-6716
23	586	27.7	116	22	US-60-160-189-10011
24	586	27.7	116	22	US-60-160-203-6200
25	586	27.7	116	22	US-60-169-840-9326
26	452.5	21.4	129	22	US-60-169-867-7998
27	451.5	21.3	128	22	US-60-195-053-1909
28	451.5	21.3	129	22	US-60-195-053-1908
29	451.5	21.3	138	22	US-60-196-718-4238
30	447.5	21.1	133	22	US-60-196-718-4237
31	416	19.7	112	22	US-60-160-203-3503
32	415.5	19.6	130	22	US-60-196-718-903
33	415	19.6	134	22	US-60-192-739-3226
34	403	19.0	104	22	US-60-160-189-5792
35	389	18.4	115	22	US-60-196-718-3944
36	388	18.3	68	22	US-60-163-123-1859
37	388	18.3	68	22	US-60-163-123-1859
38	254	12.0	75	22	US-60-188-162-5010
39	247.5	11.7	135	22	US-60-196-718-4486
40	247.5	11.7	1124	22	US-60-191-637-1341
41	247.5	11.5	1124	22	US-60-191-637-1341
42	243.5	11.5	97	22	US-60-188-162-3972
43	243.5	11.5	101	22	US-60-188-162-3971
44	237	11.2	67	10	US-08-637-021A-8
45	236.5	11.2	86	22	US-60-196-174-862

ALIGNMENTS

RESULT 1
US-09-119-209-2
: Sequence 2, Application US/09119209
: GENERAL INFORMATION:
: APPLICANT: LASKY, LAURENCE A.
: APPLICANT: STACHELL, SCOTT E.
: APPLICANT: ROSEN, STEVEN D.
: APPLICANT: SINGER, MARK S.
: APPLICANT: YEDNOCK, TED A.
: TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESS: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/119, 209
: FILING DATE: 20-Jul-1998
: CLASSIFICATION:
: PRIOR APPLICATION DATA:

Sequence 2, Appl1
Sequence 523, App
Sequence 428, App
Sequence 1751, App
Sequence 4, Appl1
Sequence 4, Appl1
Sequence 467, App
Sequence 19, Appl1
Sequence 2, Appl1
Sequence 3, Appl1
Sequence 89, Appl1
Sequence 8687, App
Sequence 5823, App
Sequence 5003, App
Sequence 6716, App
Sequence 10011, A
Sequence 6200, App
Sequence 9326, App
Sequence 7998, App
Sequence 4236, App
Sequence 1909, App
Sequence 1908, App
Sequence 4238, App
Sequence 4237, App
Sequence 3503, App
Sequence 903, App
Sequence 3226, App
Sequence 5792, App
Sequence 3944, App
Sequence 1859, App
Sequence 4179, App
Sequence 5010, App
Sequence 4486, App
Sequence 1341, App
Sequence 1056, App
Sequence 3972, App
Sequence 3971, App
Sequence 8, Appl1
Sequence 862, App

APPLICATION NUMBER: 08/513278
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/059027
FILING DATE: 6-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/786149
FILING DATE: 31-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/315015
FILING DATE: 23-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0565D1C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
us-09-119-209-2

Query Match 100.0%; Score 2116; DB 15; Length 372;
Best Local Similarity 100.0%; Pred. No. 7.2e-177;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIFPMKQSTORDLWNIFFKMGWMLCCDFLAHGGTCWTHYSEKPMWQARARFCRDN 60
DB 1 MIFPMKQSTORDLWNIFFKMGWMLCCDFLAHGGTCWTHYSEKPMWQARARFCRDN 60
QY 61 YTDVAIQKAEIEYLEKTLPSRSYVWIGIRKIGIWTWGTNKSLEAEENMGDGEPN 120
DB 61 YTDVAIQKAEIEYLEKTLPSRSYVWIGIRKIGIWTWGTNKSLEAEENMGDGEPN 120
QY 121 NKKNEDECEIYIKRKNKAGKNDACHKRLKALCYTASCPWSCSGHGECEVEIINNHTC 180
DB 121 NKKNEDECEIYIKRKNKAGKNDACHKRLKALCYTASCPWSCSGHGECEVEIINNHTC 180
QY 181 NCDVGYGPOCOLVIOCEPLAPELGTMDCTHPGNSFSSQCAFSCSEGTNLGIEETT 240
DB 181 NCDVGYGPOCOLVIOCEPLAPELGTMDCTHPGNSFSSQCAFSCSEGTNLGIEETT 240
QY 241 CGPFGMWSSPEPTCOVIOCEPLAPDLGIMNCSHPLASFSTSACTFICSGTELLIGKKK 300
DB 241 CGPFGMWSSPEPTCOVIOCEPLAPDLGIMNCSHPLASFSTSACTFICSGTELLIGKKK 300
QY 301 TICSSGIMSNPSPICKLDSFSMIKREGDYNPLFIPIVAVWVTFSGLAFLIWLARLKK 360
DB 301 TICSSGIMSNPSPICKLDSFSMIKREGDYNPLFIPIVAVWVTFSGLAFLIWLARLKK 360
QY 361 GKSKRSMNDPY 372
DB 361 GKSKRSMNDPY 372

RESULT 2

PCT-US92-03970-2
Sequence 2, Application PC/TUS9203970
GENERAL INFORMATION:
APPLICANT: Dana-Farber Cancer Institute, Inc.
TITLE OF INVENTION: LEUKOCYTE-ASSOCIATED CELL SURFACE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.

ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03970
FILING DATE: 19920513
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Heine, Holliday C.
REGISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: DECI-152Bq9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEFAX: (617) 451-0313
TELEX: 940675
INFORMATION FOR SRO. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: protein
PCT-US92-03970-2

Query Match 98.1%; Score 2076; DB 1; Length 385;
Best Local Similarity 98.1%; Pred. No. 2.4e-173;
Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MIFPMKQSTORDLWNIFFKMGWMLCCDFLAHGGTCWTHYSEKPMWQARARFCRDN 60
DB 14 MIFPMKQSTORDLWNIFFKMGWMLCCDFLAHGGTCWTHYSEKPMWQARARFCRDN 73
QY 61 YTDVAIQKAEIEYLEKTLPSRSYVWIGIRKIGIWTWGTNKSLEAEENMGDGEPN 120
DB 74 YTDVAIQKAEIEYLEKTLPSRSYVWIGIRKIGIWTWGTNKSLEAEENMGDGEPN 133
QY 121 NKKNEDECEIYIKRKNKAGKNDACHKRLKALCYTASCPWSCSGHGECEVEIINNHTC 180
DB 134 NKKNEDECEIYIKRKNKAGKNDACHKRLKALCYTASCPWSCSGHGECEVEIINNHTC 193
QY 181 NCDVGYGPOCOLVIOCEPLAPELGTMDCTHPGNSFSSQCAFSCSEGTNLGIEETT 240
DB 194 NCDVGYGPOCOLVIOCEPLAPELGTMDCTHPGNSFSSQCAFSCSEGTNLGIEETT 253
QY 241 CGPFGMWSSPEPTCOVIOCEPLAPDLGIMNCSHPLASFSTSACTFICSGTELLIGKKK 300
DB 254 CGPFGMWSSPEPTCOVIOCEPLAPDLGIMNCSHPLASFSTSACTFICSGTELLIGKKK 313
QY 301 TICSSGIMSNPSPICKLDSFSMIKREGDYNPLFIPIVAVWVTFSGLAFLIWLARLKK 360
DB 314 TICSSGIMSNPSPICKLDSFSMIKREGDYNPLFIPIVAVWVTFSGLAFLIWLARLKK 373
QY 361 GKSKRSMNDPY 372
DB 374 GKSKRSMNDPY 385

RESULT 3

PCT-US94-00909-2
Sequence 2, Application PC/TUS9400909
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: CHIMERIC SELECTINS AS STIMULANEOUS BLOCKING
AGENTS FOR COMPONENT SELECTIN FUNCTION
NUMBER OF SEQUENCES: 11
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00909
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,606
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/962,483
FILING DATE: 02-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,608
FILING DATE: 03-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/737,092
FILING DATE: 29-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/730,503
FILING DATE: 08-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/700,773
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/313,109
FILING DATE: 21-FEB-1989
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-00909-2

Query Match 98.1%; Score 2076; DB 1; Length 385;
Best Local Similarity 98.1%; Pred. No. 2.4e-173;
Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MIFPKKCGSTQDLDNINIFRLKMGWMLCCDFLAHNGTYCTHYHSEKPMNMQARRCRDN 60
DB 14 MIFPKKCGSTQDLDNINIFRLKMGWMLCCDFLAHNGTDCTHYHSEKPMNMQARRCRDN 73
QY 61 YTDVAIONKKAIEYLEKTLPSRSYVWIGIRKIGIMTWGTNKSLEFEANMGDGEFN 120
DB 74 YTDVAIONKKAIEYLEKTLPSRSYVWIGIRKIGIMTWGTNKSLEFEANMGDGEFN 133
QY 121 NKKNKEDCEVEIYIKRNKDAGKWNDDACHIKLKAALCYTASCPWSCSGHGECEVEIINNHTC 180
DB 134 NKKNKEDCEVEIYIKRNKDAGKWNDDACHIKLKAALCYTASCPWSCSGHGECEVEIINNHTC 193
QY 181 NCDVGYGPOCLVIOCEPLAPBLGIMNCSHPLASFTSACTFICSEGTTELIGKKK 240
DB 194 NCDVGYGPOCLVIOCEPLAPBLGIMNCSHPLASFTSACTFICSEGTTELIGKKK 253
QY 241 CGPFGNMSPEPTCOVIOCEPLAPBLGIMNCSHPLASFTSACTFICSEGTTELIGKKK 300
DB 254 CGPFGNMSPEPTCOVIOCEPLAPBLGIMNCSHPLASFTSACTFICSEGTTELIGKKK 313
QY 301 TICESSGIMNSNPICQKLDKSFMSIKEGDYNPFLTPVAVMVTAATSGLAFTIIMLARLKK 360
DB 314 TICESSGIMNSNPICQKLDKSFMSIKEGDYNPFLTPVAVMVTAATSGLAFTIIMLARLKK 373
QY 361 GKSKRSMDPY 372
DB 374 GKSKRSMDPY 385

RESULT 4
US-08-008-459-2
Sequence 2, Application US/08008459
GENERAL INFORMATION:
APPLICANT: Tedder, Thomas F.

APPLICANT: Kansas, Geoffrey S.
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/008,459
FILING DATE: 25-JAN-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,606
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,483
FILING DATE: 02-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,608
FILING DATE: 03-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/737,092
FILING DATE: 29-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/730,503
FILING DATE: 08-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/700,773
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/313,109
FILING DATE: 21-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Heine, Holiday C.
REGISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: DCFI-318XX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 451-0313
TELEFAX: (617) 542-2290
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-008-459-2

Query Match 98.1%; Score 2076; DB 4; Length 385;
Best Local Similarity 98.1%; Pred. No. 2.4e-173;
Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MIFPKKCGSTQDLDNINIFRLKMGWMLCCDFLAHNGTYCTHYHSEKPMNMQARRCRDN 60
DB 14 MIFPKKCGSTQDLDNINIFRLKMGWMLCCDFLAHNGTDCTHYHSEKPMNMQARRCRDN 73
QY 61 YTDVAIONKKAIEYLEKTLPSRSYVWIGIRKIGIMTWGTNKSLEFEANMGDGEFN 120
DB 74 YTDVAIONKKAIEYLEKTLPSRSYVWIGIRKIGIMTWGTNKSLEFEANMGDGEFN 133
QY 121 NKKNKEDCEVEIYIKRNKDAGKWNDDACHIKLKAALCYTASCPWSCSGHGECEVEIINNHTC 180
DB 134 NKKNKEDCEVEIYIKRNKDAGKWNDDACHIKLKAALCYTASCPWSCSGHGECEVEIINNHTC 193

QY 181 NCDVGYGPOCQVIOCEPLAEPLGTMDCTHPFGNFSSOCARFSCSEGTNLGIEETT 240
DB 194 NCDVGYGPOCQVIOCEPLAEPLGTMDCTHPFGNFNSOCARFSCSEGTNLGIEETT 253
QY 241 CGPFGMNSPEPTCOVIOCEPLASAPDLGIMNCSHPLASFSTTSACTFICSEGTLLGKK 300
DB 254 CGPFGMNSPEPTCOVIOCEPLASAPDLGIMNCSHPLASFSTTSACTFICSEGTLLGKK 313
QY 301 TICSSGIMSNPSPICQKLDKSFMSIKEDGNPLFIPAVVWTAFTSGLAFTIWLARLKK 360
DB 314 TICSSGIMSNPSPICQKLDKSFMSIKEDGNPLFIPAVVWTAFTSGLAFTIWLARLKK 373
QY 361 GKSKRSMDPY 372
DB 374 GKSKRSMDPY 385

RESULT 5
US-08-340-539-2
Sequence 2, Application US/08340539
GENERAL INFORMATION:
APPLICANT: Tedder, Thomas F.
APPLICANT: Kansas, Geoffrey S.
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
NUMBER OF INVENTIONS: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,539
FILING DATE: 16-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,606
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,483
FILING DATE: 02-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,608
FILING DATE: 03-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/737,092
FILING DATE: 29-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/730,503
FILING DATE: 08-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/700,773
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/313,109
FILING DATE: 21-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Heine, Holiday C.
REGISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: DPCI-318XX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290

TELEFAX: (617) 451-0313
TELEX: 940675
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-340-539-2

Query Match 98.1%; Score 2076; DB 7; Length 385;
Best Local Similarity 98.1%; Pred. No. 2,4e-173;
Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MIFPKCSTQTDRLNIFKLGWMTLCCDFLAHGHYCWYHYSEKPMNQRARRCRDN 60
DB 14 MIFPKCSTQTDRLNIFKLGWMTLCCDFLAHGHYCWYHYSEKPMNQRARRCRDN 73
QY 61 YTDVAIQNKAEIYELKTLDFSRSYWIGIRKIGIWTWGTNKSILTEAEWNGDGEFN 120
DB 74 YTDVAIQNKAEIYELKTLDFSRSYWIGIRKIGIWTWGTNKSILTEAEWNGDGEFN 133
QY 121 NKKKEDCEVEIYIRKNDAGKMDDACCHKLAKALCTTASCPMSGSGHCEVEIINNHTC 180
DB 134 NKKKEDCEVEIYIRKNDAGKMDDACCHKLAKALCTTASCPMSGSGHCEVEIINNHTC 193
QY 181 NCDVGYGPOCQVIOCEPLAEPLGTMDCTHPFGNFSSOCARFSCSEGTNLGIEETT 240
DB 194 NCDVGYGPOCQVIOCEPLAEPLGTMDCTHPFGNFNSOCARFSCSEGTNLGIEETT 253
QY 241 CGPFGMNSPEPTCOVIOCEPLASAPDLGIMNCSHPLASFSTTSACTFICSEGTLLGKK 300
DB 254 CGPFGMNSPEPTCOVIOCEPLASAPDLGIMNCSHPLASFSTTSACTFICSEGTLLGKK 313
QY 301 TICSSGIMSNPSPICQKLDKSFMSIKEDGNPLFIPAVVWTAFTSGLAFTIWLARLKK 360
DB 314 TICSSGIMSNPSPICQKLDKSFMSIKEDGNPLFIPAVVWTAFTSGLAFTIWLARLKK 373
QY 361 GKSKRSMDPY 372
DB 374 GKSKRSMDPY 385

RESULT 6
US-08-410-569-2
Sequence 2, Application US/08410569
GENERAL INFORMATION:
APPLICANT: Tedder, Thomas F.
APPLICANT: Spertini, Olivier G.
TITLE OF INVENTION: LEUCOCYTE ADHESION MOLECULE-1 (LAM-1)
NUMBER OF INVENTIONS: AND LIGAND THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,569
FILING DATE: 03-OCT-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,608
FILING DATE: 03-OCT-1991
APPLICATION NUMBER: US 07/700,773

FILING DATE: 15-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Helne, Holliday C.
REGISTRATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: DFCG-152EX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-2290
TELEFAX: (617) 451-0313
TELEX: 940675
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-410-569-2

Query Match 98.1%; Score 2076; DB 8; Length 385;
Best Local Similarity 98.1%; Pred. No. 2.4e-173;
Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MIFPKCSTORDLWIKKLMGWTMLCCDPLAHGCTYTHYSKPMNQARARFCND 60
DB 14 MIFPKCSTORDLWIKKLMGWTMLCCDPLAHGCTYTHYSKPMNQARARFCND 73
QY 61 YTDVAIONKAEIEYLEKTLPPSRSYWIGIRKIGITWVGTNKSLEAEENMGDEPN 120
DB 74 YTDVAIONKAEIEYLEKTLPPSRSYWIGIRKIGITWVGTNKSLEAEENMGDEPN 133
QY 121 NKKNKEDVEIYIKRKNKAGKMNDACHKLAALCYTASCPWSCSGHGECEIINNHTC 180
DB 134 NKKNKEDVEIYIKRKNKAGKMNDACHKLAALCYTASCPWSCSGHGECEIINNHTC 193
QY 181 NCDVGYRPOCOLVIOCEPLAEPLGTMDCTHPGNSFSSQCAFSGEGNLTGIEETT 240
DB 194 NCDVGYRPOCOLVIOCEPLAEPLGTMDCTHPGNSFSSQCAFSGEGNLTGIEETT 253
QY 241 CGPGNMSSPEPTCOVIOCEPLASAPDLGIMNCSHPLASFSTFISACTFICSEGTILGKK 300
DB 254 CGPGNMSSPEPTCOVIOCEPLASAPDLGIMNCSHPLASFSTFISACTFICSEGTILGKK 313
QY 301 TICSSGIMNSPPIQCKLDFSFMKEGDNPLFIPIVAVWTAESGLAFIIMLARLKK 360
DB 314 TICSSGIMNSPPIQCKLDFSFMKEGDNPLFIPIVAVWTAESGLAFIIMLARLKK 373
QY 361 GKSKRSNDPY 372
DB 374 GKSKRSNDPY 385

RESULT 7
US-60-212-659-523
Sequence 523, Application US/60212659
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000674
CURRENT APPLICATION NUMBER: US/60/212, 659
CURRENT FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 879
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 523
LENGTH: 1078
TYPE: PRT
ORGANISM: HUMAN
US-60-212-659-523

Query Match 89.0%; Score 1883; DB 22; Length 1078;
Best Local Similarity 97.4%; Pred. No. 6.5e-156;

Matches 336; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 22 GWTMLCCDPLAHGCTYTHYSKPMNQARARFCNDYTDVAIONKAEIEYLEKTL 81
DB 604 GYFLPSKDFLAHGTDCWTHYSKPMNQARARFCNDYTDVAIONKAEIEYLEKTL 663
QY 82 FRSRYWIGIRKIGITWVGTNKSLEAEENMGDEPNKKKEDVEIYIKRKNKDGK 141
DB 664 FRSRYWIGIRKIGITWVGTNKSLEAEENMGDEPNKKKEDVEIYIKRKNKDGK 723
QY 142 WNDACCHKLKAALCYTASCPWSCSGHGECEIINNHTCNCVGYRPOCOLVIOCEPLE 201
DB 724 WNDACCHKLKAALCYTASCPWSCSGHGECEIINNHTCNCVGYRPOCOLVIOCEPLE 783
QY 202 APELCTMDCTHPGNSFSSQCAFSGEGNLTGIEETTCGPGMSSPEPTCOVIOCEP 261
DB 784 APELCTMDCTHPGNSFSSQCAFSGEGNLTGIEETTCGPGMSSPEPTCOVIOCEP 843
QY 262 LSAPDLGIMNCSHPLASFSTFISACTFICSEGTILGKKKTICSSGIMNSPPIQCKL 321
DB 844 LSAPDLGIMNCSHPLASFSTFISACTFICSEGTILGKKKTICSSGIMNSPPIQCKL 903
QY 322 SFSMIKEDYNPLFIPIVAVWTAESGLAFIIMLARLKKGKSKR 366
DB 904 SFSMIKEDYNPLFIPIVAVWTAESGLAFIIMLARLKKGKSKR 948

RESULT 8
US-60-207-315-428
Sequence 428, Application US/60207315
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000601
CURRENT APPLICATION NUMBER: US/60/207, 315
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 428
LENGTH: 1078
TYPE: PRT
ORGANISM: HUMAN
US-60-207-315-428

Query Match 88.8%; Score 1879; DB 22; Length 1078;
Best Local Similarity 97.1%; Pred. No. 1.4e-155;
Matches 335; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 22 GWTMLCCDPLAHGCTYTHYSKPMNQARARFCNDYTDVAIONKAEIEYLEKTL 81
DB 604 GYFLPSKDFLAHGTDCWTHYSKPMNQARARFCNDYTDVAIONKAEIEYLEKTL 663
QY 82 FRSRYWIGIRKIGITWVGTNKSLEAEENMGDEPNKKKEDVEIYIKRKNKDGK 141
DB 664 FRSRYWIGIRKIGITWVGTNKSLEAEENMGDEPNKKKEDVEIYIKRKNKDGK 723
QY 142 WNDACCHKLKAALCYTASCPWSCSGHGECEIINNHTCNCVGYRPOCOLVIOCEPLE 201
DB 724 WNDACCHKLKAALCYTASCPWSCSGHGECEIINNHTCNCVGYRPOCOLVIOCEPLE 783
QY 202 APELCTMDCTHPGNSFSSQCAFSGEGNLTGIEETTCGPGMSSPEPTCOVIOCEP 261
DB 784 APELCTMDCTHPGNSFSSQCAFSGEGNLTGIEETTCGPGMSSPEPTCOVIOCEP 843
QY 262 LSAPDLGIMNCSHPLASFSTFISACTFICSEGTILGKKKTICSSGIMNSPPIQCKL 321
DB 844 LSAPDLGIMNCSHPLASFSTFISACTFICSEGTILGKKKTICSSGIMNSPPIQCKL 903
QY 322 SFSMIKEDYNPLFIPIVAVWTAESGLAFIIMLARLKKGKSKR 366
DB 904 SFSMIKEDYNPLFIPIVAVWTAESGLAFIIMLARLKKGKSKR 948

Db 904 SFSMIKEDYNPFLIPVAVMTAFSGLAFLIWLARLKKGKRSKR 948

RESULT 9

US-60-230-435-1751

Sequence 1751, Application US/60230435

GENERAL INFORMATION:

APPLICANT: Beasley, Ellen

TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEIN,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: C1000768

CURRENT APPLICATION NUMBER: US/60/230,435

CURRENT FILING DATE: 2000-09-06

NUMBER OF SEQ ID NOS: 2991

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1751

LENGTH: 1078

TYPE: PRT

ORGANISM: HUMAN

US-60-230-435-1751

Query Match 88.8%; Score 1879; DB 22; Length 1078;

Best Local Similarity 97.1%; Pred. No. 1,4e-155;

Matches 335; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 22 GWTMLCDEFLAHGTYCWTYHSEKPMNORARRCRNITDVAIQKAEIYELEKTL 81

Db 604 GYELSPKDEFLAHGTDCTYHSEKPMNORARRCRNITDVAIQKAEIYELEKTL 663

QY 82 FSRSYTWIGIRKIGIWTWGTNKLTEAEKWDGDEPNKKKNEDEVEIYIKRNKDAK 141

Db 664 FSRSYTWIGIRKIGIWTWGTNKLTEAEKWDGDEPNKKKNEDEVEIYIKRNKDAK 723

QY 142 WNDACHLKAALCYTASCPMSCSGHGECEIINNHTCNDVYGPQCOLVIOCEPLE 201

Db 724 WNDACHLKAALCYTASCPMSCSGHGECEIINNHTCNDVYGPQCOLVIOCEPLE 783

QY 202 APELGTMDCTHPFGNFSFSSQAFSCSEGTNLGIEETTCGPFGNWSSPEPTCQVIOCEP 261

Db 784 APELGTMDCTHPFGNFSFSSQAFSCSEGTNLGIEETTCGPFGNWSSPEPTCQVIOCEP 843

QY 262 LSAIDLGMNCSHPLASFTSACTFICSEGTIELIGKKTICSSGSIWNSPICOGLDK 321

Db 844 LSAIDLGMNCSHPLASFTSACTFICSEGTIELIGKKTICSSGSIWNSPICOGLDK 903

QY 322 SFSMIKEDYNPFLIPVAVMTAFSGLAFLIWLARLKKGKRSKR 366

Db 904 SFSMIKEDYNPFLIPVAVMTAFSGLAFLIWLARLKKGKRSKR 948

RESULT 10

US-09-119-209-4

Sequence 4, Application US/09119209

GENERAL INFORMATION:

APPLICANT: LASKY, LAURENCE A.

APPLICANT: STACHELL, SCOTT E.

APPLICANT: ROSEN, STEVEN D.

APPLICANT: SINGER, MARK S.

APPLICANT: YEDNOCK, TED A.

TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/119,209

FILING DATE: 20-Jul-1998

CLASSIFICATION:

Prior Application DATA:

APPLICATION NUMBER: 08/513278

FILING DATE: 10-Aug-1995

Prior Application DATA:

APPLICATION NUMBER: 08/059027

FILING DATE: 6-MAY-1993

Prior Application DATA:

APPLICATION NUMBER: 07/786149

FILING DATE: 31-OCT-1991

Prior Application DATA:

APPLICATION NUMBER: 07/315015

FILING DATE: 23-FEB-1989

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P0565D1C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5530

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 372 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-09-119-209-4

Query Match 78.0%; Score 1651; DB 15; Length 372;

Best Local Similarity 76.1%; Pred. No. 3.6e-136;

Matches 283; Conservative 32; Mismatches 57; Indels 0; Gaps 0;

QY 1 MIPPMKQSTQFQDMLNIFKMGWMLCDEFLAHGTYCWTYHSEKPMNORARRCFCDN 60

Db 1 MVEPMKEGTWMSRNILKLMWTLCCFLHGHGHTYHSEKPMNENARFCFKN 60

QY 61 YTDVAIQKAEIYELEKTLPEFSRSYTWIGIRKIGIWTWGTNKLTEAEKWDGDEPN 120

Db 61 YTDVAIQKAEIYELEKTLPEFSRSYTWIGIRKIGIWTWGTNKLTEAEKWDGDEPN 120

QY 121 NKNKEDCEVEIYIKRKDKGKWNDDACHLKAALCYTASCPMSCSGHGECEIINNHTC 180

Db 121 NKNKEDCEVEIYIKRKDKGKWNDDACHLKAALCYTASCPMSCSGHGECEIINNHTC 180

QY 181 NCDVYGPQCOLVIOCEPLEAPELGTMDCTHPFGNFSFSSQAFSCSEGTNLGIEETT 240

Db 181 ICDAGYGPQCYVVOCEPLEAPELGTMDCTHPFGNFSFSSQAFSCSEGTNLGIEETT 240

QY 241 CGPFGNWSPEPTCQVIOCEPLSAPDLGIMNCSHPLASFTSACTFICSEGTIELIGKR 300

Db 241 CGASGNWSSPEPTCQVIOCEPLSAPDLGIMNCSHPLASFTSACTFICSEGTIELIGKR 300

QY 301 TICSSGSIWNSPICOGLDKSFSMIKEDYNPFLIPVAVMTAFSGLAFLIWLARLKK 360

Db 301 TOGASGNWSSPEPTCQVIOCEPLSAPDLGIMNCSHPLASFTSACTFICSEGTIELIGKR 360

QY 361 GKSKRSMDPY 372

Db 361 GKSKRSMDPY 372

RESULT 11

PCT-US94-09395-4

Sequence 4, Application PC/TUS9409395

GENERAL INFORMATION:

APPLICANT: Board of Regents of the University of Oklahoma

TITLE OF INVENTION: Expression Control Sequences of the P-Selectin Gene

NUMBER OF SEQUENCES: 17

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Patricia L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-4530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09395
FILING DATE: 19-AUG-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-815-6508
TELEFAX: (404)-815-6555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 830 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US94-09395-4

```

Query Match	42.8%	Score 905	DB 1	Length 830
Best Local Similarity	50.6%	Pred. No. 1.9e-70		
Matches 157	Conservative 47	Mismatches 106	Indels 0	Gaps 0

Qy	8	OSTORDMINIEKILGMMILCCDFLAHNGTCMYTHAESEKPMNOBARFCRDYTDLVAI	67
Dd	11	QRPQVAVFGISOLLCSFALLISELNOKEVAAWMTYHSTKAVSNMISKYYQONKRTDLVAI	70
Qy	68	ONKEIEYLEKTLPLFSMSYYWTGTRGGTWIWTGNTKSLTEAEANNGDEPNNKKKED	127
Dd	71	QONKEIIDYLNKVLTYESSYYWIGIRKNNKKTWTWTGTRKALTNEENADNEPNNKRNED	130
Qy	128	CVEIYIRKKNKDGKMNDDACHKILAAALCYTASCOPMSCSGHCEVEITINNHGTNCDDGY	187
Dd	131	CVEIYIKSPAPKGMNDEHCLKKKNHALCYTASCODMSCSNQGBELERIGWYTCSCYGEY	190
Qy	188	GPOCQVLYIOCEPRLAPBLGTMDCTHPNGNFSFSQCAFSCSEGTNLTGIEETTCGPPGMN	247
Dd	191	GPECEYVAREGEELRLPHVLMVINCNSHPNGNFSFSQCSFHTDGYQVNGPSKLCCLASGIW	250
Qy	248	SSPEPTCOVIOCEPRLAPADLGIMNCSHPRLASFSTYSACFTICSBGRLICKKRTICSSG	307
Dd	251	TNKRPOCLAQCPRLKIRPENGNMICLISAKAFQHOSSCSFSCBEGFALVDEPYVQCTASG	310
Qy	308	TWSNPSTICO	317
Dd	311	WTRAPAPVCK	320

RESULT 12
US-08-449-687B-4
Sequence 4, Application US/08449687B
GENERAL INFORMATION:
APPLICANT: Mcever, Rodger P.
APPLICANT: Pan, Junliang
TITLE OF INVENTION: Expression Control sequences of the
TITLE OF INVENTION: P-Selectin Gene
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Patricia L. Pabst
STREET: 2800 One Atlantic Center

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US-08-449-687B-4

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QY	308 TWSNPSPICQ 317					
Dd	311 VMTAPAPVCX 320					

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RESULT 13
US-60-207-315-467
; Sequence 467, Application US/60207315
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEIN,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF

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[illegible]

OY 219 FSSQCAFSCSEGTNLTGIEFTTCGPEGNMSSPEPTQVIOCEPLSAPDDGIMNCSPILAS 278
Db 202 YNSSCSISCDRGLPSSMETMQCMSSGEMSAPIPACNVECDAVTNPANGFVECFONPGS 261
OY 279 FSTTSACTFICSEGTIELGKKKTTICSSSGIWSNPSPICQ 317
Db 262 FPMNTTCTFDCDEEGFELMGASLOCTSSGNMNDNEKPTCK 300

Search completed: January 13, 2001, 01:56:54
Job time: 4781 sec

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OM of: US-09-119-209-2 to: GenEmbl: * out_format: pfs

Date: Jan 13, 2001 3:07 AM

About: Results were produced by the GenCore software, version 4.5.
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -CGAPOP=4.500
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-DELEXT=7.000 -START=1 -MATRIX=blsnum62 -TRANS=human40.cdl
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Search Information block:

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Query length: 372

Database: GenEmbl: *

Database sequences: 1118133

Database length: -1736092196

Search time (sec): 1246.430000

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gb_pat1:MMPLNHR	+ 2110.00	3310.82	2.9e-175	2259	X16070 Human mRNA for pln hom
gb_pat1:HUMLNHR	+ 2094.00	3285.19	7.9e-175	2354	M2580 Human lymph node homing
gb_pat1:USA246000	+ 2090.00	3282.49	1.1e-174	1569	AJ246000 Homo sapiens mRNA for
gb_pat1:PTU3728	+ 2085.00	3277.62	2.1e-174	1119	U73728 Pan troglodytes L-select
gb_pat1:HSLEU8	+ 2082.00	3266.37	8.8e-174	2323	X16150 Human mRNA for leu-8 p
gb_pat1:HSLEYA1	+ 2076.00	3256.87	3.0e-173	2330	X16150 Human lymph node homing
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gb_pat1:BTLECAM1	+ 1695.00	2653.06	9.9e-140	2650	X62882 B. taurus mRNA for LECAM
gb_pat1:579523	+ 1667.00	2614.68	1.8e-137	1580	S79523 lymphocyte membrane p
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gb_pat1:AR060685	+ 858.50	1331.67	5.1e-66	3351	L25527 Rattus norvegicus E-
gb_pat1:BOVESLECT	+ 857.00	1330.55	5.9e-66	2911	M87862 Mus musculus E-select
gb_pat1:MUSLECAM1B	+ 857.00	1328.27	7.9e-66	3759	M80778 Mouse ELAM-1 gene, c
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VERSION	AR060685.1 GI:5987135				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 2259)				
AUTHORS	Lasky, L.A., Rosen, S.D., Stachel, S.E. and Slinger, M.S.				
TITLE	Soluble lymphocyte homing receptors				
JOURNAL	Patent: US 5840844-A 1 24-NOV-1998;				
FEATURES	Location/Qualifiers				
SOURCE	1..2259				
BASE COUNT	635 a 517 c 488 g 619 t				
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Ratio: 5.68 Gaps: 0
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transmembrane protein.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 2259)
AUTHORS Bowen,B.R., Nguyen,T. and Lasky,L.A.
TITLE Characterization of a human homologue of the murine peripheral

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JOURNAL Lymph node homing receptor
MEDLINE J Cell Biol. 109 (1), 421-427 (1989)
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ACCESSION M25280
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2354)

AUTHORS Siegelman, M. H. and Weissman, I. L.
TITLE Human homologue of mouse lymph node homing receptor: evolutionary conservation at tandem cell interaction domains
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 86 (14), 5562-5566 (1989)
MEDLINE 89315837
COMMENT Draft entry and computer-readable sequence for [1] kindly provided by M.H. Siegelman, 02-JUN-1989.
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Thesis (1998) Freie Universitaet Berlin, Fachbereich Chemie
2 (bases 1 to 1569)
Fieger C.B.
Direct Submission
Submitted (04-SEP-1999) Fieger C.B., Benjamin Franklin Klinikum der
Freien Universitaet Berlin, Institut fuer Klinische Chemie &
Pathobiochemie, Hindenburgdamm 30, 12200 Berlin, GERMANY
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REFERENCE  1 (bases 1 to 1119)
AUTHORS    Budman,J.I., Fu,H., Johnson,C.E., Thakur,A.B., Berg,E.L. and
            Tsurushita,N.
TITLE      Cloning of the cDNA encoding L-selectin from nonhuman primates
JOURNAL    Unpublished
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AUTHORS    Budman,J.I., Fu,H., Johnson,C.E., Thakur,A.B., Berg,E.L. and
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VERSION X17519.1 GI:34344

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SOURCE human.

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REFERENCE 1 (bases 1 to 2323)

AUTHORS Camerini,D., James,S.P., Stamenkovic,I. and Seed,B.

TITLE Leu-8/TOI is the human equivalent of the Mel-14 lymph node homing receptor

JOURNAL Nature 342 (6245), 78-82 (1989)

MEDLINE 90044046

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ACCESSION  X16150
VERSION    X16150.1 GI:34428
KEYWORDS   cell surface protein; leukocyte adhesion protein; transmembrane
SOURCE     human.
ORGANISM   Homo sapiens
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REFERENCE  1 (bases 1 to 2330)
            Tedder, T. F.
            Direct Submission
            Submitted (09-NOV-1989) Tedder T. F.
            2 (bases 1 to 2330)
            Tedder, T. F., Isaacs, C. M., Ernst, T. J., Demetri, G. D., Adler, D. A. and
            Distchech, C. M.
            Isolation and chromosomal localization of cDNAs encoding a novel
            human lymphocyte cell surface molecule, LAM-1. Homology with the
            mouse lymphocyte homing receptor and other human adhesion proteins
            J. Exp. Med. 170 (1), 123-133 (1989)
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ACCESSION AR016679
VERSION AR016679.1 GI:3972956
KEYWORDS
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  1 (bases 1 to 2330)
  AUTHORS Tedder, T. F. and Spertini, O. G.
  TITLE Anti-LAM 1-3 antibody and hybridoma
  JOURNAL Patent: US 5776775-A 1 07-JUL-1998;
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DEFINITION Sequence 1 from patent US 5808025.
ACCESSION AR040718
VERSION AR040718.1 GI:5960081
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS Tedder, T. F. and Kansas, G. S.
TITLE Chimeric selectins as simultaneous blocking agents for component
JOURNAL Patent: US 5808025-A 1 15-SEP-1998;
FEATURES
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ACCESSION AR054061
VERSION AR054061.1 GI:5978923
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SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2330)
AUTHORS Tedder, T.F. and Kansas, G.S.
TITLE Use of chimeric selectins as simultaneous blocking agents for
JOURNAL component selectin function
FEATURES
source Location/Qualifiers
BASE COUNT 661 a 522 c 487 g 660 t
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ACCESSION 170140
VERSION 170140.1 GI:3006275
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 2330)
AUTHORS Tedder, R.F. and Spertini, O.G.
TITLES Methods of blocking adhesion with anti-Lam1-3 antibody
JOURNAL Patent: US 5679346-A, 1 21-OCT-1997;
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DEFINITION Pongo pygmaeus L-selectin mRNA, complete cds.
ACCESSION U73729
VERSION 073729.1 GI:1658017
KEYWORDS
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ORGANISM
Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.
REFERENCE
1 (bases 1 to 1119)
Budman,J.I., Fu,H., Johnson,C.E., Thakur,A.B., Berg,E.L. and
Tsurushtita,N.
Cloning of the cDNA encoding L-selectin from nonhuman primates
2 (bases 1 to 1119)
Budman,J.I., Fu,H., Johnson,C.E., Thakur,A.B., Berg,E.L. and
Tsurushtita,N.
Direct Submission
Submitted (08-OCT-1996) Protein Design Labs, Inc., 2375 Garcia
Avenue, Mountain View, CA 94043, USA
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1 (bases 1 to 1119)
Hudman,J.I., Fu,H., Johnson,C.E., Thakur,A.B., Berg,E.L. and
Tsurushita,N.
Cloning of the cDNA encoding L-selectin from nonhuman primates
unpublished
2 (bases 1 to 1119)
Budman,J.I., Fu,H., Johnson,C.E., Thakur,A.B., Berg,E.L. and
Tsurushita,N.
Direct Submission
Submitted (08-OCT-1996) Protein Design Labs, Inc., 2375 Garcia
Avenue, Mountain View, CA 94043, USA
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Cercopithecinae; Papio.
REFERENCE
AUTHORS Tsunushita,N., Fu,H. and Berg,E.L.
JOURNAL PCR cloning of the cDNA encoding baboon L-selectin
MEDLINE 97128794
REFERENCE
AUTHORS Tsunushita,N.
JOURNAL Direct Submission
JOURNAL Submitted (21-MAR-1996) Naoya Tsunushita, Protein Design Labs,
Inc., 2375 Garcia Avenue, Mountain View, CA 94043, USA
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Copyright (c) 1993-2000 CompuGen Ltd.

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-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blsum62
-TRANS=human40.cdi -LIST=45 -DOCCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORW=ext -MINLEN=0 -MAXLEN=2000000000
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Search information block:

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Query Length: 372
Database: N_Geneseq_36:*
Database sequences: 480022
Database length: 187831343
Search time (sec): 89.970000

score_list:

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/cg2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:181217				2082.00	3003.56	1.6e-159
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seq_documentation_block:

ID Q43154 standard; cDNA; 2259 BP.

AC Q43154;

DT 08-OCT-1993 (first entry)

DE Human Lymphocyte Homing Receptor coding sequence.

KW HuLHR; Lymphocyte binding inhibition; Lymphoma metastasis;

KW Transplant rejection; ss.

XX Homo sapiens.

PH Key Location/Qualifiers

FT CDS 129..1247

FT /*tag= a

FT /product= HuLHR

FT sig_peptide 186..224

FT /*tag= b

PN US5216131-A.

PD 01-JUN-1993.

PR 23-FEB-1989; 89US-0315015.

PR 23-FEB-1989; 89US-0315015.

PR 31-OCT-1991; 91US-0786149.

PA (GENE) GENENTECH INC.

PI Lasky LA, Rosen SD, Singer MS, Stachel SE, Yednock TA;

WP1: 1993-188588/23.

P-PSDB; R37960.

PT Human and murine lymphocyte homing receptors to treat graft

PS rejection and inflammation - comprise carbohydrate binding,

XX epidermal growth factor and complement binding domains

XX Example 2; Fig 1; 32pp; English.

CC A human peripheral blood lymphocyte cDNA library in lambda gt10 was

CC screened with a 2.2kb EcoRI Insert of the murine Mel1a antigen clone

CC (1.e. a murine LHR sequence). The largest EcoRI Insert (2.2kb) was

CC isolated and sequenced. The ORF codes for 372 amino acids with a mol.

CC wt. of approximately 42,200. Comparison of the HuLHR cDNA with the

CC previously determined murine LHR sequence (Q43155) showed 83%

CC homology.

XX Sequence 2259 BP; 635 A; 515 C; 490 G; 619 T; 0 other;

alignment_scores:

Quality: 2116.00 Length: 372

Percent Similarity: 100.000 Gaps: 0

Percent Identity: 100.000

Alignment block:

US-09-119-209-2 x Q43154 ..

Align seg 1/1 to: Q43154 from: 1 to: 2259

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17 ephelLysLeuTrpGlyTrpThrMetLeuCysCysAspPheLeuAlaHisH 34
179 CTTCAGATGTGGGGGTGGACAAATGCTCTGTGTGATTCCTGGGCATTC 228
34 IsGlyThrYrCysTrpThrYrHisTyrSerGluLysProMetAsnTrp 50
229 ATGGAACTACTGCTGCTGACTTACCATTAATTCGAAACCAATGAACTGG 278
51 GlnArgAlaArgArgPheCysArgAspAsnTyrThrAspLeuValAlaI 67
279 CAAAGGGCTAGAAAGATTCTGCCAGACAAATTACACAGATTAGTGGCAT 328
67 eGlnAsnLysAlaGluIleGluTyrLeuGluLysThrLeuProPheSerA 84
329 ACAAAACAAGGCGGAATGTGAGTATCTGAGAAAGACTGCGCTTCAGTC 378
84 rGserTyrTrpTrpIleGlyIleArgLysIleGlyLysIleTrpThrTrp 100
379 GTTCTTACTACTGATAGAAATCCGGAAGATAGAGAAATATGACACTGG 428
101 ValGlyThrAsnLysSerLeuThrGluGluAlaGluAsnTrpGlyAspG 117
429 GTGGGACCAACAATCTCTCACTGAGAGACAGAACTGGGGAGATGG 478
117 yGluProAsnAsnLysLysAsnLysGluAspCysValGluIleTyrIle 134
479 TGAAGCCCAACAAGAACAGACAGAGAGACTGCGTGGAGATCTATATCA 528
134 yArgAsnLysAspAlaGlyLysTrpAsnAspAlaCysHisLysLeu 150
529 AAGAGAAACAAGATGACGCAATGCAACGATGACGCCCTGCCACAAACTA 578
151 LysAlaAlaLeuCysTyrThrAlaSerCysGluProTrpSerCysSerG 167
579 AAGGACAGCCCTCTGTACACAGCTTCTGCCAGCCCTGGTACAGAGTGG 628
167 yHisGlyLysCysValGluIleIleAsnAsnHisThrCysAsnCysAsp 184
629 CCATGGAGAAATGTGTAAGAAATCATCAATATCACAACCTGCAACTGTATG 678
184 aGlyTyrTyrGlyProGlnCysGlnLeuValIleGlnCysGluProLeu 200
679 TGGGGTACTATGGGCCCACTGCTGAGCTTGATTCAGTGTGAGCCCTTGG 728
201 GluAlaProGluLeuGlyThrMetAspCysThrHisProPheGlyAsnPh 217
729 GAGGCCCAAGACTGGGTACCATGAGCTGTACTACCCCTTTGGAACTT 778
217 eSerPheSerSerGlnCysAlaPheSerCysSerGluGlyThrAsnLeuT 234
779 CAGCTTCAGCTACAGTGTGCTTCACTGCTGTGAGAACCAAACTTAA 828
234 hArgYIleGluGluThrThrCysGlyProPheGlyAsnTrpSerSerPro 250
829 CTGGGATTGAGAAACCACTGCTGACCATTTGGAACTGCTCATCTCCA 878
251 GluProThrCysGlnValIleGlnCysGluProLeuSerAlaProAspLe 267
879 GACCAACCTGTCAAGTATTCAGTGTGAGCTCTATCAGACACAGATTT 928
267 uGlyIleMetAsnCysSerHisProLeuAlaSerPheSerPheThrSerA 284
929 GGGGATCATGAAGTACCATCCCTGGCAGCTTCAGCTTACCTCTG 978
284 IacYsthrPheIleCysSerGluGlyThrGluLeuIleGlyLysLysLys 300
979 CATGTACCTTATCTGCTCAGAAAGAACTGAGTTAATTGGGAGAAAGAAA 1028
301 ThrIleCysGluSerSerGlyIleTrpSerAsnProSerProIleCysG 317
|||||

1029 ACCATTGTGAAATCATCTGGAATCTGTCAAACTCTAGTCCAAATATGTCA 1078
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1079 AAAAATTGGACAAAGTTTCTCATGATTTAAGAGGGGTGATTTAAACCCC 1128
334 euPheIleProValAlaValMetValIleAlaPheSerGlyLeuAlaPhe 350
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351 IleIleTTrpLeuAlaArgArgLeuLysLysGlyLysLysSerLysArgse 367
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seq_documentation_block:
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XX
AC Q44243:
XX
DT 11-JAN-1994 (first entry)
XX
DE HULHR DNA.
XX
KW Human; murine; lymphocyte; cell surface glycoprotein; homing receptor;
LHR; endothelium; lymphoid tissue; signal; domain; complement binding;
carbohydrate binding; epidermal growth factor-like; egf; intracellular;
KW transmembrane binding; cytoplasmic; ligand binding partner protein;
TMD; LBPP; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 129..1247
FT FT /*tag= a
FT sig_peptide 186..224
FT /*tag= b
FT mat_peptide 243..1244
FT /*tag= c
XX
PN US522538-A.
XX
PD 06-JUL-1993.
XX
PF 23-FEB-1989; 89US-0315015.
XX
PR 23-FEB-1989; 89US-0315015.
PR 22-NOV-1989; 89US-0440625.
PR 16-DEC-1991; 91US-0808122.
XX
PA (GENETH) GENENTECH INC.
XX
PI Capon DJ, Lasky LA;
XX
DR WPI: 1993-226664/28.
DR P-PSDB: R38908.
XX
PT New lymphocyte homing receptor immunoglobulin fusion
PT polypeptide(s) - used to inhibit binding of lymphocytes in
PT therapeutic and diagnostic uses
XX
PS Disclosure: Fig 1; 44pp; English.
XX
CC The sequences given in Q44243-44 encode human and murine lymphocyte
CC cell surface glycoprotein (LHR) respectively. The proteins encoded
CC by these sequences mediate the binding of lymphocytes to the
CC endothelium of lymphoid tissue. LHR is a glycoprotein which contains
CC a signal domain, a carbohydrate binding domain, an epidermal growth

CC factor-like (egf) domain, at least one complement binding domain
 CC repeat, a transmembrane binding domain (TMD) and a charged intra-
 CC cellular or cytoplasmic domain. The murine and human amino acid
 CC sequences show a high degree of overall homology (83%), however
 CC degrees of homology between the various domains is variable. These
 CC proteins may be fused to a ligand binding partner protein (LBP) which
 CC causes an increase in the half life of the LHR. The fusions may be
 CC used therapeutically to compete with the normal binding of
 CC lymphocytes to lymphoid tissue. They may be used in organ or graft
 CC rejection and for the treatment of inflammation.

XX
 SO Sequence 2259 BP: 635 A: 516 C: 489 G: 619 T: 0 other:

alignment_scores:

Quality: 2116.00 Length: 372
 Ratio: 5.688 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-119-209-2 x 044243 ..

Align seg 1/1 to: 044243 from: 1 to: 2259

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34 IeGIYThrCYSTrPrTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrp50
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229 ATGGAACCTACTGCTGCTGACTTACCATTTATTCGAAAACCCATGAC278
51 GlnArgAlaArgArgPheCysArgAspAsnTrpTrpAspLeuValAla1 67
|||||
279 CAAAGGGCTAGAAAGATTCTGCCGAGACAAATACACAGATTGATGCCAT328
67 eGlnAsnLysAlaGluIleGluTrpLeuGluLysThrLeuProPheSerA 84
|||||
329 ACAAACAGAGCGGAATTGATATCTGGAGAAACTCTGCCCTTCAGAGC378
84 IYSerTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrp100
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117 YGluProAsnAsnLysLysAsnLysGluAspCysValGluIleTrpIle134
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134 YSArGAsnLysAspAlaGlyLysTrpAsnAspAlaCysHisLysLeu150
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151 LysAlaAlaLeuCYSTrTrpThrAlaSerCysGlnProTrpSerCysSerC167
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184 aIGLYTrpCYGlyPrGlnCysGlnLeuValIleGlnCysGlnProLeu200
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679 TGGGTACTATGGCCCAAGTGTCAAGCTTGATGATTCAGTGTAGCCCTTGG728
201 GluAlaProGluLeuGlyThrMetAspCysThrHisProPheGlyAsnPh217

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779 CAGCTTCACCTCACAAGTGTCCCTTCAGCTGTCTGGAAGAACAAACTTAA828
234 hGlyIleGluGluPheTrpThrCysGlyProPheGlyAsnTrpSerSerPro250
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251 GluProThrCysGlnValIleGlnCysGluProLeuSerAlaProAspLe267
|||||
879 GAACCAACCTGTCAAGTGAATCAGTGTGAGCCCTCTATCAGACACCAAT928
267 uGlyIleMetLeuAsnCysSerHisProLeuAlaSerPheSerPheThrSerA284
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XX
AC 092802;
XX
DT 01-DEC-1995 (first entry)
XX
DE Human LHR cDNA.
XX
KW Lymphocyte homing receptor; lymphocyte cell surface glycoprotein;
KW LHR; ligand binding partner; immunoglobulin; constant region;
KW antibody engineering; immunomodulator; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 129..1247
FT FT /*tag= a
FT sig_peptide 186..224
FT FT /*tag= b
FT mat_peptide 243..1244
FT FT /*tag= c
XX
PN US5428130-A.
XX
PD 27-JUN-1995.
XX
PF 23-FEB-1989; 89US-0315015.

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XX 22-NOV-1989; 89US-0440625.
PR 23-FEB-1989; 89US-0315015.
PR 16-DEC-1991; 91US-0808122.
PR 08-DEC-1992; 92US-0986931.
XX
PA (GETH) GENENTECH INC.
XX
PI Capon DJ, Lasky LA;
XX
DR WPI: 1995-240086/31.
DR P-PSDB; R76506.
XX
PT New hybrid ligand binding partner molecules - fused to immunoglobulin
PT constant region sequences to increase stability and in vivo plasma
XX half-life
PS Disclosure: Fig. 1a-1c; 40pp; English.
XX
CC A murine Mel 14 antigen cDNA clone was used to screen a lambda gt10
CC cDNA library derived from human peripheral blood lymphocyte mRNA
CC obtd. from primary cells. A cDNA clone encoding LHR was isolated.
XX
SQ Sequence 2255 BP; 635 A; 516 C; 489 G; 619 T; 0 other;

alignment_scores:

Quality: 2116.00 Length: 372
Ratio: 5.688 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-119-209-2 x 092802 ..

Align seg 1/1 to: 092802 from: 1 to: 2259

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17 ephelAsleuTrpGlyTrpHmetLeuScyAspPheLeuAlaHisH 34
179 CTTCAACTCTGGGGGTGGAGCATCTCTGTTGATTTCTCGCACATC 228
34 IsGlyHTrpLyScyTrpHTrpHisTyrSerGluLysProMetAsnTrp 50
229 ATGGAACCTACTGCTGCTGACTTACCATTTATCGAAAAACCATGAACTGG 278
51 GlnArgAlaArgArpPheCysArgAspAsnTrpTrpAspLeuValAlaI 67
279 CAAGAGGCTAGAAAGATTCTGCCGAGACAAATTACACAGATTGATGGCCAT 328
67 eGlnAsnLysAlaGluIleGluTyrLeuGluLysThrLeuProPheSerA 84
329 ACMAAACAGGCGGAAATTCATCTCATCTGAGAGACACTCTGCCCTTCAGTC 378
84 rGSerTyrTrpIleGlyIleArgLysIleGlyValIleTyrTrp 100
379 GTTCTTACTACTGATAGCATCCGGAAGATGAGAGAAATGAGACCTGG 428
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429 GTGGAGACCAACAATCTCTCAGTGAAGACAGACAGAACCTGGGGAGATGG 478
117 yGluProAsnAsnLysLysAsnLysGluAspCysValGluIleTyrIle 134
479 TGAGCCCAACAACAAGAAACAAGAGAGAGACTCGTGGAGATCTATATCA 528
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629 CCATGAGAAATGTGTAGAAATCATCAATATACACACCTGCACACTGTGATG 678
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679 TGGGGTACTGTGGGCCCCAGTGTACGTTGTGATTCAGTGTGAGCCTTGG 728
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729 GAGGCCCCAGAGCTGGTACCAATGACATGTACTCTACCCCTTTGAAACTP 778
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267 uGlyTleMetAsnCysSerHisProLeuAlaSerPheSerPheTrpSerA 284
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284 IaCysTrpPheIleCysSerGlyGlyThrGluLeuIleGlyLysLys 300
979 CATGTACCTTCATCTGCTCAGAGAACTGAGTATATTGGAGAAAGAAA 1028
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317 nLysLeuAspLysSerPheSerMetIleLysGluLysAspTyrAsnPro 334
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334 eupHeIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
1129 TCTTCATTCAGTGGAGATGATGATTTACTGCAATCTCTGGGTTGGCATTT 1178
351 IleIleTrpLeuAlaArgArgLeuLysLysGlyLysLysSerLysArg 367
1179 ATCATTTGGCTGGCAAGAGATTTAAAAAAGCAAGAAATCCAAAGAGAAC 1228
367 rMetAsnAspProTyr 372
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seq_name: /cgm2_2/gcgdata3/geneseq/geneseq/NA1995.DAT:705869

seq_documentation_block:

ID 705869 standard: cDNA: 2259 BP.

AC 705869;

DT 31-JAN-1996 (first entry)

DE Human LHR cDNA.

XX

Lymphocyte cell surface glycoprotein; LHR: transmembrane receptor;

KW immunoglobulin; IgG: constant region; receptor-mediated disease;

OS

XX Homo sapiens.

PH

Location/Qualifiers

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FT CDS 129..1247
FT /*Cag= a
FT sig_peptide 186..224
FT /*Cag= b
FT mat_peptide 243..1244
FT /*Cag= c
FT /product= LHR
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XX US5455165-A.
XX
XX 03-OCT-1995.
XX
XX 23-FEB-1989; 89US-0315015.
XX
XX 22-NOV-1989; 89US-0440625.
XX 23-FEB-1989; 89US-0315015.
XX 16-DEC-1991; 91US-0808122.
XX 08-DEC-1992; 92US-0986931.
XX 21-JAN-1994; 94US-0185669.
XX
XX (SETH ) GENENTECH INC.
XX
XX Capon DJ, Lasky LA:
XX WPI; 1995-350776/45.
XX P-PSDB; R83050.
XX
XX Expression vector encoding fusion protein to increase plasma life -
XX PT treatment of receptor mediated disease
XX
XX PS Disclosure; Fig 1; 42pp; English.
XX
XX A mouse LHR (lymphocyte cell surface glycoprotein) cDNA clone was used
XX CC to screen an oligo-dT primed lambda gt10 cDNA library derived from
XX CC human peripheral blood lymphocyte mRNA obtd. from primary cells. A
XX 2.2 kb clone (sequence given in T05869) showing 83% DNA sequence
XX CC homology to the murine LHR gene (T05870) was isolated. The LHR genes
XX CC are used to construct LHR-IgG hybrids used to target therapeutic
XX CC moieties to lymphoid tissue.
XX
XX Sequence 2259 BP; 635 A; 516 C; 489 G; 619 T; 0 other:

Alignment_scores:
    Quality: 2116.00      Length: 372
    Ratio: 5.688          Gaps: 0
    Percent Similarity: 100.000      Percent Identity: 100.000

Alignment_block:
US-09-119-209-2 x T05869 ..

Align seg 1/1 to: T05869 from: 1 to: 2259

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17 ePheLysLeuTrpGlyTrpThrMetLeuCysCysAspPheLeuAlaIsh 34
   |||||
179 CTTCAGCTGTTCGGGGTGGACAAATGCTCTGTTCGATTTCCTCGCCACATC 228
   |||||
34 IsgLTThrCysTrpThrTrpThrHisTyrSerGlnLysProMetAsnTrp 50
   |||||
229 ATGGAACTTACTGCTGGACTTACCACTATTCTGAAAAACCCATGAACTGG 278
   |||||
51 GlnArgAlaArgArgPheCysArgAspAsnTyrThrAspLeuValAla1 67
   |||||
279 CAAGAGGCTAGAGATTCTCGCCGAGACAAATTACACAGATTATGTTGCCAT 328
   |||||
67 eGlnAsnLysAlaGluIleGlyTyrLeuGluLysThrLeuProPheSerA 84
   |||||
329 ACAAAACAAGCGCAAAATTGAGTATCTCGAGAAAGACTCTGCCCTTCAGTGC 378
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84 rSerTyrTyrTrpIleGlyIleArgLysIleGlyGlyIleTrpThrTrp 100
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151 LysAlaAlaLeuCysTyrThrAlaSerCysGlnProTrpSerCysSerG1 167
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629 CCATGGAGAAATGTGTAGAATCATCAATATACACACACTGCACACTGTGAG 678
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1179 ATCATTTTGGCTGGCAAGGAGATTTAAAAAAGCAGAAATTCACAAGAGAAC 1228
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367 rMetAsnAspProTyr 372
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1229 TATGAATGACCCATAT 1244
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seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1996.DAT:T30003

seq_documentation_block:

ID T30003 standard; DNA: 2259 BP.

AC T30003;

XX 31-OCT-1996 (first entry)

XX Human lymphocyte cell surface glycoprotein (HULHR) coding sequence.

XX Immunoglobulin; transmembrane receptor; adhesion; targeting;
 KW diagnosis; therapy; drug delivery; antiviral; neuromodulator;
 KW immunomodulator; cell adhesion; graft rejection; inflammation;
 KW metastasis; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 129..1247

FT sig_peptide 129..242 /product= Lymphocyte cell surface glycoprotein.

FT mat_peptide 243..1244

FT /tag= b

FT /tag= c

XX US5514582-A.

XX 07-MAY-1996.

XX 23-FEB-1989; 89US-0315015.

XX 22-NOV-1989; 89US-0440625.

XX 23-FEB-1989; 89US-0315015.

XX 16-DEC-1991; 91US-0808122.

XX 08-DEC-1992; 92US-0986931.

XX 21-JAN-1994; 94US-0185670.

XX (GETH) GENENTECH INC.

XX Capon DJ, Lasky LA;

XX WPI: 1996-238773/24.

XX P-PSDB: R98106.

XX Nucleic acid encoding hybrid immunoglobulin comprising the ligand

XX binding site of a receptor fused to Ig constant region - useful for

XX diagnosis and treatment e.g. of inflammation

XX Example 2; Figure 1; 41pp; English.

XX A hybrid immunoglobulin chain comprising the ligand binding site of
 CC a single transmembrane receptor without an active transmembrane
 CC region; fused at its C-terminus with the N-terminus of an
 CC immunoglobulin constant region. The receptor is not a member of the
 CC immunoglobulin super family, nor a multiple subunit polypeptide
 CC encoded by discrete genes. The hybrid immunoglobulin chain combines
 CC effector functions of immunoglobulin and can bind to and/or activate
 CC more than one ligand. It can be used diagnostically for the in
 CC vitro assay of LBP and their targets; or therapeutically to deliver
 CC LBP such as toxins, enzymes, growth factors to particular cells.
 CC Typical applications are as antiviral, neuromodulating and
 CC immunomodulating agents, or as modulators of cell adhesion (e.g. in
 CC treating graft rejection; inflammation; metastasis of lymphoma etc.)
 CC The immunoglobulin component increases plasma half life and
 CC facilitates purification while deletion of the transmembrane region
 CC potentially immunogenic epitopes.

XX Sequence 2259 BP; 635 A; 516 C; 489 G; 619 T; 0 other;

alignment_scores:

Quality: 2116.00

Ratio: 5.688

Percent Similarity: 100.000

Percent Identity: 100.000

alignment_block:

US-09-119-209-2 x T30003 ..

Align seg 1/1 to: T30003 from: 1 to: 2259

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34 IsGlyThrTrpCysTrpThrTrpHisTyrSerGluLysProMetAsnTrp 50
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479 TGAGCCCAACAACAAGAAAGAAAGAGAGACTCTGAGATCTATATCA 528
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151 LysAlaAlaLeuCysTyrThrAlaSerCysGlnProTrpSerCysSerG 167
579 AAGCAGCCCTCTGTACACAGCTTCTGCCAGCCCTGGTCATGACGTGG 628
167 yHisGlyGluCysValGluIleLeuAsnAsnHisTrpCysAsnCysAspY 184
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seq_name: /cgn2.2/gcdata/geneseq/geneseqn/NA1998.DAT.V19012

seq_documentation_block:

ID V19012 standard; DNA: 2259 BP.

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XX AC V19012:
XX DT 17-AUG-1998 (first entry)
XX DE Homo sapiens lymphocyte homing receptor (LHR) gene.
XX KW Lymphocyte homing receptor; LHR; HuLHR; organ; graft; rejection;
KW treatment; inflammatory disorders; rheumatoid arthritis;
KW autoimmune diseases; lymphoma metastasis; control; lymphocyte;
KW accumulation; ds.
XX OS Homo sapiens.
XX FI Key Location/Qualifiers
XX FT CDS 129..1247
XX FT /tag= a
XX FT /product= lymphocyte homing receptor
XX PN US5714147-A.
XX PD 03-FEB-1998.
XX PF 23-FEB-1989; 89US-0315015.
XX PR 22-NOV-1989; 89US-0440625.
XX PR 23-FEB-1989; 89US-0315015.
XX PR 19-DEC-1991; 91US-0808122.
XX PR 08-DEC-1992; 92US-0986931.
XX PR 21-JAN-1994; 94US-0185670.
XX PR 26-MAY-1995; 95US-0451848.
XX PA (GETH ) GENENTECH INC.
XX PI Capon DJ, Lasky LA;
XX DR WPI; 1998-129805/12.
XX P-PSDB; W37781.
XX

```

PT Prevention of lymphocyte attachment to endothelial cells - using
PT chimeric molecule comprising lymphocyte homing receptor and
PT immunoglobulin constant region
XX
PS Disclosure: Fig 1; 43pp; English.

XX
CC The sequence is that encoding a human lymphocyte homing receptor
CC (LHR) which may be used in the construction of a chimeric molecule
CC comprising an LHR fused at its C terminus to the N terminus of an
CC immunoglobulin constant region. This can be used for the prevention
CC of lymphocyte attachment to endothelial cells. Such a method may
CC be used for preventing organ or graft rejection, for treating
CC inflammatory disorders, e.g. rheumatoid arthritis or other
CC autoimmune diseases, for controlling lymphoma metastasis and
CC for treating conditions in which there is an accumulation of
CC lymphocytes.

XX Sequence 2259 BP: 635 A; 516 C; 489 G; 619 T; 0 other:

alignment_scores:

Quality:	Ratio:	Length:	Gaps:
2116.00	5.688	372	0
Percent Similarity: 100.000	Percent Identity: 100.000		

alignment_block:

US-09-119-209-2 x V19012

Align seg 1/1 to: V19012 from: 1 to: 2259

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34 lSGlyThrTrpCysTrpThrTrpHisTyrSerGluLysProMetAsnTrp 50
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729 GAGGCCCGAGAGCTGGTACCATGAGCTGACCTCCACCCCTTGGAAACTT 778
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267 uGlyIleMetAsnCysSerHisProLeuAlaSerPheSerPheThrSera 284
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seq_documentation_block:
ID V08321 standard: DNA; 2259 BP.
XX
AC V08321:
XX
DT 02-FEB-1999 (first entry)
XX
DE Human lymphocyte homing receptor coding sequence.
XX
KW Lymphocyte homing receptor; LHR; lymphocyte cell-surface glycoprotein;
KW lymphocyte binding; endothelium; graft rejection; inflammation; therapy;
KW arthritis; autoimmune disease; lymphoma metastasis;
KW lymphocyte accumulation; human; ss.
XX
OS Homo sapiens.
XX
PN US5840844-A.
XX
PD 24-NOV-1998.
XX
PF 10-AUG-1995; 95US-0513278.
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PR 23-FEB-1989; 89US-0315015.
PR 31-OCT-1991; 91US-0786149.
PR 06-MAY-1993; 93US-0059029.
PR 10-AUG-1995; 95US-0513278.
XX
XX (GETH ) GENENTECH INC.
XX (REGC ) UNIV CALIFORNIA.
XX
PI Lasky LA, Rosen SD, Singer MS, Stachel SE;
XX WPL; 1999-034122/03.
XX DR P-PSDB; W73264.
XX
XX Lymphocyte homing receptor polypeptides - useful for inhibiting
XX lymphocyte binding to lymphoid endothelium
XX
XX Disclosure; Fig 1; 33pp; English.
XX
XX This sequence encodes the human lymphocyte homing receptor (LHR) of the
XX invention. LHR is a lymphocyte cell-surface glycoprotein that mediates
XX the binding of lymphocytes to the endothelium of lymphoid tissue. Soluble
XX LHR polypeptides, lacking signal peptide (amino acids 1-38),
XX transmembrane domain (amino acids 333-355) and cytoplasmic domain (amino
XX acids 356-372), can be used therapeutically to compete with the normal
XX binding of lymphocytes to lymphoid tissue and are especially useful for
XX organ or graft rejection treatment protocols, for treating inflammatory
XX diseases such as arthritis and other autoimmune diseases, for control of lymphoma
XX metastasis and for treating conditions involving lymphocyte accumulation.
XX LHR polypeptides can also be used in assays for LHR, anti-LHR antibodies
XX or competitive inhibitors of LHR activity, and for purifying anti-LHR
XX antibodies, and as immunogens for raising anti-LHR antibodies.
XX
SO Sequence 2259 BP; 635 A; 517 C; 488 G; 619 T; 0 other.
XX
alignment_scores:
Quality: 2116.00 Length: 372
Ratio: 5.688 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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US-09-119-209-2 x V08321 ..
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279 CAAAGGCGTAGAAAGATTCTGCCGAGACAATTACACAGATTATGTTGCCAT 328
67 eGlnAsnLysAlaGluIleGlyTyrLeuGluLysThrLeuProPheSera 84
329 ACMAAACAAGGCGGAATTTGAGTATCTGAGAGACACTGCGCTTCAGTC 378
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379 GTTCTTACTACTGATAGGAATCCGAGAGATAGAGGAATATGACCTGCG 428
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679 TGGGGTACTATGGGCCCCAGTGTCACTGTGATTGATTCAGTGTGAGCCTTTG 728
201 GIAlaIleProGluLeuGlyThrMetAspCysThrHisProPhcGlyAsnPh 217
|||||
729 GAGGCCCCAGAGCTGGGTGACATGAGACTGTACTACACCCCTTGGAACCTT 778
217 eSerPheserSerGlnCysAlaPheserCysSerGlnGlyThrAsnLeuT 234
|||||
779 CAGCTTCACGCTCACAGTGTGCTTCAAGTGTCTGAGAACAAACCTTAA 828
234 hGlyIleGlnGluThrThrCysGlyProPhcGlyAsnTrpSerSerPro 250
|||||
829 CTGGGATTGAGAGMAAACACACTGTGAGACCTTTGGAACGTGATCTCCA 878
251 GIuProThrCysGlnValIleGlnCysGlnProLeuSerAlaProAspLe 267
|||||
879 GAACCAACCTGTCAAGTCAATTCAGTGTGAGCCTTATCAGCACACGATTTC 928
267 uGlyIleMetAsnCysSerHisProLeuAlaSerPheserPhetnSerA 284
|||||
929 GCGGATCATGAACTGTAGCCATCCCTGGCCAGCTTCACACTTTACTCTCG 978
284 IaCysThrPheIleCysSerGlnGlyThrGluLeuIleGlyLysLysLys 300
|||||
979 CATGTACCTTCACTGTCTCAGAAAGAACAGTGAATTATGGGAAGAA 1028
301 ThrIleCysGlnSerSerGlyIleTrpSerAsnProSerProIleCysGI 317
|||||
1029 ACCATTTGTGAATCAATCTGCAATCTGTCAAAATCCTAGTCCAAATATGTCA 1078
317 nLysLeuAspLysSerPheserMetIleLysGlnGlyAspTyrAsnProL 334
|||||
1079 AAAATTTGCACAAAGTTTCTCATATGATTAAGAGAGGCTCATTTAAACCCC 1128
334 euPheIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
|||||
1129 TCTTCATTCAGAGTGGCAGTCAATGATTGATCTCTGGGTGGCATATT 1178
351 IleIleTrpLeuAlaIleArgLeuLysGlyLysLysSerLysArgSe 367
|||||
1179 ATCATTTTGGCTGGCAAGAGATTAAAAAAAGGCAAGAAATCCACAGAGAG 1228
367 rMetAsnAspProTyr 372
|||||
1229 TATGAATGACCCATAT 1244
seq_name: /cgn2_2/gcndata/geneseq/geneseqn/NA1992.DAT.Q24987
seq_documentation_block:
ID Q24987 standard: DNA; 2262 BP.
XX
AC Q24987;
XX
DT 22-NOV-1992 (first entry)
XX
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```
DE Sequence encoding human lymphocyte cell surface glycoprotein
DE (HuLHR).
XX
KW Lymphocyte cell surface glycoprotein; ligand binding protein; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 129..185
FT sig_peptide /*tag= a
FT mat_peptide 186..242
FT /*tag= b
FT 143..1247
FT /*tag= c
XX
FN US5116964-A.
XX
PD 26-MAY-1992.
XX
PE 22-NOV-1989; 89US-0440625.
XX
PR 23-FEB-1989; 89US-0315015.
PR 22-NOV-1989; 89US-0440625.
XX
PA (GETH ) GENENTECH INC.
XX
PI Capon DJ, Lasky LA.
XX
DR WPI: 1992-199589/24.
DR P-PSDB: R24026.
XX
PT Nucleic acid encoding polypeptide fusions - comprising ligand
PT binding partner protein and immunoglobulin chain, for use in
PT diagnosis and therapy
XX
PS
XX
PS Disclosure: Fig 1-1 - 1-3; 43pp; English.
XX
CC LHR mediates the binding of lymphocytes to the endothelium of
CC lymphoid tissue. Full length cDNA clones and DNA encoding the human
CC and the murine LHR (HuLHR and MLHR, respectively) have been
CC identified and isolated (see Q24987 and Q24988). LHR is a
CC glycoprotein which contains the following protein domains: a signal
CC sequence, a carbohydrate binding domain, and epidermal growth
CC factor-like (egf) domain, at least one and preferably two complement
CC binding domain repeat, a transmembrane binding domain (TMD), and a
CC charged intracellular or cytoplasmic domain. LHR is used as the
CC ligand-binding partner in fusion polypeptides with an immunoglobulin,
CC for use in diagnosis and therapy.
XX
SO Sequence 2262 BP; 635 A; 518 C; 488 G; 621 T; 0 other;

alignment_scores:
Quality: 2109.00 Length: 372
Ratio: 5.685 Gaps: 0
Percent Similarity: 99.731 Percent Identity: 99.731

alignment_block:
US-09-119-209-2 x Q24987
Align seg 1/1 to: Q24987 from: 1 to: 2262

1 MetIlePheProTrpLysCysGlnSerThrGlnArgAspLeuTrpAsnIle 17
|||||
129 ATGATATTTTCCATGAGAAATGTCAGAGCACCCAGAGGACTTATGCAACAT 178
17 ePheLysLeuTrpGIYTrpThrMetLeuCysCysAspPheLeuAlaHisH 34
|||||
179 CTTCAGATTGTGGGGGTGACAAATGCTCTGTGTGATTTTCTGGCAGATC 228
34 IsGIYThrTyrCysTrpThrTyrHisTyrSerGlnLysPheMetAsnTrp 50
|||||
229 ATGGAACCTACTGCTGAGACTTACATTAATTATCTGMAAAACCATGAACTGG 278
```

```

51  GlnArgAlaArgArgPheCysArgAspAsnTyrThrAspLeuValAlaIle 67
279  CAAGGGCTAGAGATTCCTGCCACACATTTACACAGATTTAGTGGCCAT 328
67  eGlnAsnLysAlaGluIleGluTyrLeuGluTyrThrLeuProPheSer 84
329  ACAAAACCAAGCGGAAATGAGATATCTGGAAGAAGCTGCGCCCTCAGTC 378
84  rGSetTyrTyrTrpIleGlyIleArgLysIleGlyIleLeuPheTrp 100
379  GTTCTTACTACTGATGAGATCCGGAACATAGAGAGATATGACGCTGG 428
101  ValGlyThrAsnLysSerLeuThrGluValGluAsnTyrPglYaspG 117
429  GTGGAGACCAACAATCTCTCAGTGAAGAGCGAGAACTGGGAGATGG 478
117  yGluProAsnAsnLysLysAsnLysGluAspCysValGluIleTyrIle 134
479  TGAGCCCAACAACAAGAACAGAGAGAGCTGGGTGAGATCTATATCA 528
134  yArgAsnLysAspAlaGlyLysTrpAsnAspAlaCysHisLysLeu 150
529  AGAGAAACAAGATGCAAGCAAAATGAAACGATGACCCCTGCCACAAC 578
151  LysAlaAlaLeuCysTyrThrAlaSerCysGlnProTrpSerCysSer 167
579  AAGGAGCCCTCTGTACACAGCTTCTTGCACGCCCTGATCAGTCAGTG 628
167  yHisGlyGluCysValGluIleLeuAsnAsnHisThrCysAsnCysAsp 184
629  CCATGAGAAATGTGTAGAAATCATCATATATCAACCTGCACACTGTG 678
184  aIGlyTyrTyrGlyProGlnCysGlnLeuValIleGlnCysGluProLeu 200
679  TGGGCTACTATGGCCCCAGTGTGACGTGTGTGATTCAGTGTGAGCTTT 728
201  GluAlaProGluLeuGlyThrMetAspCysThrHisProPheGlyYasn 217
729  GAGGCCCAAGCTGGGTACATGACATGACTGACACCCCTTTGGAAACT 778
217  eSerPheSerSerGlnCysAlaPheSerCysSerGluGlyThrAsnLeu 234
779  CACCTTCAGCTCACAGTGTGCTCAGCTGCTGAGAGAACAACTTAA 828
234  hGlyIleGluGluTyrThrCysGlyProPheGlyYasnTrpSerPro 250
829  CTGGGATGAAAGAAACACCTGTGACCATTTGGAACTGGTCACTTCCA 878
251  GluProThrCysGlnValIleGlnCysGluProLeuSerAlaProAsp 267
879  GAACCAACTGTCAAGTATTCAGTGTAGCCCTCATACAGCACCAAGATT 928
267  uGlyIleMetAsnCysSerHisProLeuAlaSerPheSerPheSer 284
929  GGGGATTCATGAACCTGACCATCCCTGGCCAGCTTCAAGCTTACCTCG 978
284  JacTyrThrPheIleCysSerGluGlyThrGluLeuIleGlyLysLys 300
979  CATGTACCTTCATCTGTCACAAGAACTAGCTTAATTGGGAAGAAACAA 1028
301  ThrIleCysGluSerSerGlyIleTrpSerAsnProSerProIleCys 317
1029  ACCATTGTGATATCATCTGGAATGTGCTCAAAATCTAGTCCATATGTCA 1078
317  nLysLeuAspLysSerPheSerMetIleLysGluGlyAspTyrAspPro 334
1079  AAAATTTGGACAAAAGTTTCTCAATGATTAGGAGGATGATTAACCCCC 1128
334  eupHeleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
1129  TCTTCATTTCCAGTGGCAGTCACTGTTACTGCAATTCCTGGTGGCATTT 1178

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351  IleIlePheLeuAlaArgArgLeuLysLysGlyLysSerLysArgSe 367
1179  ATCATTTGGCTGGCAGAGATTAATAAAAGCAAGAAATCAAGAGAAG 1228
367  rMetAsnAspProTyr 372
1229  TATGAATGACCCCATAT 1244

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seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1992.DAT:Q23623

seq_documentation_block:

ID Q23623 standard; DNA; 2260 BP.

AC Q23623;

DT 01-SEP-1992 (first entry)

DE Human lymphocyte homing receptor gene.

DE HULHR; LHR; binding; endothelium; immunogens; graft; organ; ss;

KW rejection; inflammation; rheumatoid arthritis; lymphoma metastasis.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 129..1248

XX /tag= a

PN US5098833-A.

XX 24-MAR-1992.

PD 23-FEB-1989; 89US-0315015.

XX 23-FEB-1989; 89US-0315015.

XX (REGC) UNIV OF CALIFORNIA.

PA Lasky LA, Rosen SD, Stachel SE, Singer MS, Yednock TA;

PI WPI: 1992-123385/15.

XX P-PSDB; R22802.

DR New DNA encoding at least one domain of lymphocyte homing

PT receptor - useful for treating graft rejection, inflammation,

PT etc.

XX Claim 3; Fig 1; 32pp; English.

PS The DNA sequence was obt'd. by screening an oligo dT primed lambda

CC g10 cDNA library derived from human peripheral blood lymphocyte

CC mRNA obt'd. from primary cells, with a 2.2 kb EcoRI insert of the

CC murine Mel 14 antigen cDNA clone. 12 positive plaques were isolated

CC and those with the largest EcoRI insert were sequenced. The 2.2 kb

CC clone encodes an open reading frame of 372 amino acids. The human

CC LHR is 83 percent homologous with the murine LHR sequence and

CC contains regions encoding a carbohydrate binding domain, an EGF-like

CC domain, a complement binding domain and a transmembrane domain.

CC Cells transformed by the hLHR DNA are used to produce LHR (which

CC mediates binding of lymphocytes to the endothelium of lymphoid

CC tissue). LHR or its variants are useful as reagents for assaying

CC LHR or anti-LHR antibodies, to purify the antibodies, as immunogens,

CC (to prevent graft/organ rejection; to treat inflammation (such as

CC rheumatoid arthritis or other autoimmune diseases); for control of

CC lymphocyte metastasis, and to treat conditions associated with

CC accumulation of lymphocytes). Derivs. and variants of LHR may be

CC produced having modified properties, e.g. increased activity, longer

CC plasma half-life, reduced side effects and better ag. solubility.

CC See also Q23624 and Q23464.

XX Sequence 2260 BP; 636 A; 518 C; 487 G; 619 T; 0 other;

alignment_scores:

Quality: 2108.00 Length: 372
 Ratio: 5.667 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 99.462

alignment_block:

US-09-119-209-2 x Q23623 ..

Align seg 1/1 to: Q23623 from: 1 to: 2260

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1 MetLlePheProTrpLysCysGlnSerThrGlnArgAspLeuTrpAsn11 17
  |||
129 ATGATATTTTCATGTGAATAATGTCAGACACCACAGCGACTTATGGAACAT 178
  |||
17 ePheLysLeuTrpGlyTrpThrMetLeuCysAspPheLeuAlaHis34 34
  |||
179 CTTCAGATTGTGGGCTGGACAATGCTGTGTCTGATTTCTGGCACATC 228
  |||
34 1AGlyThrTyrcysTrpThrTyrcHisTyrSerGluLysProMetAsnTrp 50
  |||
229 ATGGAACTCCTACTGCTGACTTACCATTATTCTGAAACCCATGACTGG 278
  |||
51 GlnArgAlaArgArgPheCysArgAspAsnTyrThrAspLeuValAla1 67
  |||
279 CAACGCGTACGAAGATCTGCCGAGACAATTCACAGATTAGTTGCCAT 328
  |||
67 eGlnAsnLysAlaGluLleGluTrleuGluLysThrLeuProPheSerA 84
  |||
329 ACAAAACAAGCGCGAATATGAGTATCTGGAGAGACTCTGCCCTTCAGTC 378
  |||
84 rGserTyrTyrTrpLleGlyLleArgLysIleGlyLysIleTrrpThrTP 100
  |||
379 GTTCTTACTACTGATAGGAATCCGGAATAGAGGAATATGGACGTGG 428
  |||
101 ValGlyThrAsnLysSerLeuThrGluAlaGluAsnTrpGlyAspG1 117
  |||
429 GTGGCAACCAACAATCTCTCACTGAAGCAAGCAACTGGGAGATCG 478
  |||
117 yGluProAsnAsnLysLysAsnLysGluAsnLysValGluIleTyrIle1 134
  |||
479 TCAGCCCAACAACAAGAGAACAGACGAGCGCGTGAGATCTTAATATCA 528
  |||
134 yArgGlnLysAspAlaGlyLysTrpAsnAspAspAlaCysHisLysLeu 150
  |||
529 AGGAAACAAGAATGCGCAAAATGGAACGATGACGCTGCCCAAAACTA 578
  |||
151 LysAlaAlaLeuCysTyrTrpAlaSerCysGlnProTrpSerCysSerG1 167
  |||
579 AAGCGAGCCCTCTGTACACAGCTTCTTCCAGCCCTGTCATGACGTGG 628
  |||
167 yHisGlyGluCysValGluIleIleAsnAsnHisThrCysAsnCysAspY 184
  |||
629 CCAATGGAGAATGTGAAGAATCATCAATATCACACCTTCACTGTGATG 678
  |||
184 aIGlyTyrTrpGlyProGlnCysGlnLeuValIleGlnCysGluProLeu 200
  |||
679 TGGGGTACTATGGGCCCCAGTGTCACTGTGATTCAGTGTGAGCCTTTG 728
  |||
201 GluAlaProGluLeuGlyThrMetAspCysThrHisProPheGlyAsnPh 217
  |||
729 GAGGCCCCAGACCTGGGTACATGAGCTGTACTCAACCCCTTTGAAACT 778
  |||
217 eSerPheSerSerGlnCysAlaPheSerCysSerGluGlyThrAsnLeuT 234
  |||
779 CAGCTTCACACTCACAGTGTGCTTCAGCTGTCTGAAGCAACAACCTTAA 828
  |||
234 hrcGlyLleGluGluTrpThrCysGlyProPheGlyAsnTrpSerSerPro 250
  |||
828 CTGGGATTTAAGAAACCACTGTGAGCACTTTGGAAACTGGTCATCTCCA 878
  |||
251 GluProThrCysGlnValIleGlnCysGluProLeuSerAlaProAsp1 267
  |||
  
```

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879 GAACAACCTGTCAAGTATTCAGTGTGAGCCTCTATCAACACACAGATTTT 928
267 uGlyIleMetLysCysSerHisProLeuAlaSerPheSerPheThrSerA 284
  |||
929 GGGGATCATGAACTGTAGCCATCCCTGGCAGCTTCAAGCTTACCTCTG 978
  |||
284 1AcysThrPheLecysSerGluGlyThrGluLeuIleGlyLysLysLys 300
  |||
979 CATGTACCTTCATCTGCTCAGAAAGAACTGAGTTATTTGGGAACAAGAA 1028
  |||
301 ThrIleCysGluSerSerGlyIleTrrpSerAsnProSerProIleCysG1 317
  |||
1029 ACCATTTGTGAATCAATCTGGAATCTGTCAAAATCTCAGTCCAAATATG 1078
  |||
317 nLysLeuAspLysSerPheSerMetLleLysGluGlyAspTyrAsnProL 334
  |||
1079 AATATTGGACAAATGTTTCTCAATGATTTAAGAGGCTGATTATTAACCCC 1128
  |||
334 ePheLleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
  |||
1129 TCTTCATTCACAGTGGCAGATGATGTTACTGCAATTTCTGGGTTGGCAT 1178
  |||
351 IleIleTrrpLeuAlaArgArgLeuLysGlyLysLysSerLysArgse 367
  |||
1179 ATCATTTTGGCTGGCAAGAGATTTAAAAAAGCAAGAAATCCAAAGAGAG 1228
  |||
367 rMetAsnAspProTyr 372
  |||
1229 TATGAATGACCCATAT 1244
  |||
seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1991.DAT:012118
seq_documentation_block:
ID Q12118 standard; DNA: 2259 BP.
XX
XX Q12118:
XX
XX 09-SEP-1991 (first entry)
XX
DE Sequence encoding human lymphocyte cell surface glycoprotein (LHR).
KW Ligand binding partner; lbp: stable plasma protein; spp: antiviral;
KW immunomodulatory; neuromodulatory; receptor mediated abnormality; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 129..1247
FT /*tag= a
FT sig_peptide 186..224
FT /*tag= b
FT mat_peptide 243..1244
FT /*tag= c
XX
XX MO9108298-A.
XX
XX PD 13-JUN-1991.
XX
XX PF 21-NOV-1990; 90WO-US06849.
XX
XX PR 22-NOV-1989; 89US-0444625.
XX
XX (GETH ) GENENTECH INC.
XX
XX Capon DJ, Tasky LA:
XX
XX WPI: 1991-193202/26.
XX
XX P-PSDB: R12469.
XX
XX New hybrid immunoglobulin(s) - for use as diagnostic reagents for
XX ligand binding molecules and to treat organ and graft rejection
XX and inflammation.
XX
  
```

PS Disclosure: Fig 1; 67pp: English.
 XX
 CC The gene product may be used as a ligand binding partner in combina-
 CC tion with a stable plasma protein eg IgG1-IgG4, IgA, IgE, IgD or IgM.
 CC The fusion product is joined by N- or C-terminal groups, preferably
 CC the N-terminal of the Fc region of the ssp is linked to the C-terminal
 CC of Ibp. They may be used to provide antiviral, immunomodulatory
 CC and neuromodulatory treatment as well as in treatment of receptor
 CC mediated abnormalities.
 XX
 SQ Sequence 2259 BP; 634 A; 516 C; 487 G; 618 T; 4 other:

alignment_scores:

Quality: 2095.00 Length: 372
 Ratio: 5.662 Gaps: 0
 Percent Similarity: 99.462 Percent Identity: 99.462

alignment_block:

US-09-119-209-2 x Q12118 ..

Align seg 1/1 to: Q12118 from: 1 to: 2259

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1 MetIlePheProTrpLysCysGlnSerThrGlnArgAspLeuTrpAsnIle 17
|||||
129 ATGATATTTCATGSAATGTCAAGCACGCCAGAGGGCTTATGGAACAT 178
|||||
17 ePheLysLeuTrpGlyTrpThrMetLeuCysCysAspPheLeuAlaHis 34
|||||
179 CTTCAGATTGTGGGGGTGGACAATGCTGTGTGTGATTTCCTGGCAATC 228
|||||
34 ISGlyThrTrpCysTrpThrTrpHisTrpSerGluYspPrometAsnTrp 50
|||||
229 ATGGAACCTACTGCTGACACTTACCATATTCTGAAAAACCATGAATCG 278
|||||
51 GlnArgAlaArgArgPheCysArgAspAsnTrpThrAspLeuValAlaI 67
|||||
279 CAAGGGCTAGAAAGATTCTCCCGACAAATTACACAGATTATTGCGCAT 328
|||||
67 eGlnAsnLysAlaGluIleGluTrpLeuGluYspThrLeuProPheSera 84
|||||
329 ACAAAACAAGCCGGAATTTGATATCTGGAGAACTCTGCCCTTCAGTC 378
|||||
84 rGserTrpTrpIleGlyIleArgLysIleGlyIleTrpTrpTrp 100
|||||
379 GTTCTTACTACTGATAGGAATCCGGAATAGAGAAATATGAGAGTGG 428
|||||
101 ValGlyThrAsnLysSerLeuThrGluAlaGluAsnTrpGlyAspGlu 117
|||||
429 GTGGGAACCAACAATCTCTCACTGAAGAAGCAGAACTGGGAGATGG 478
|||||
117 yGluProAsnAsnLysLysAsnLysGluAspCysValGluIleTrpIle 134
|||||
479 TGAGCCCAACAACAAGACAGACAGAGACNGCGTGAGATCTATATCA 528
|||||
134 yArgAsnLysAspAlaGlyLysTrpAsnAspAspAlaCysHisLysLeu 150
|||||
529 AGGAAACAACAAGATGCAAGCAATGGAACGATGAGCCTGCACACAACT 578
|||||
151 LysAlaAlaLeuCysTrpThrAlaSerCysGlnProTrpSerCysSerGlu 167
|||||
579 AAGGACGCCCTCTGTACACAGACTTCTTGCCAGCCCTGTGTATGACAGTGG 628
|||||
167 yHisGlyLysCysValGluIleAsnAsnHisThrCysAsnCysAspVal 184
|||||
629 CCATGAGAAATGTGTAGAAATCATCAATATATCACACCTGCACACTGTATG 678
|||||
184 aGlyTrpTrpGlyProGlnCysGlnLeuValIleGlnCysGluProLeu 200
|||||
679 TGGGTTACTATGGGCCCAAGTGTGAGCTTGTGATTCAGTGTGAGCCCTTGG 728
|||||
201 GluAlaProGluLeuGlyThrMetAspCysThrHisProGlyAsnPh 217
|||||

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729 GAGGCCCCAGAGCTGGGTACCATGAGACTGTACTACACCCCTTGGAAACTT 778
217 eSerPheSerSerGlnCysAlaPheSerCysSerGluGlyThrAsnLeuTr 234
|||||
779 CAGTTCAAGTCACTACAGATGTGCTTCAAGCTGCTGTGAAGGACAAACTTAA 828
234 hrcGlyIleGluGluTrpThrCysGlyProPheGlyAsnTrpSerSerPro 250
|||||
829 CTGGGATTGAAAGAAACCACTGTGGACCATTTGGAACTGGTCACTCTCA 878
251 GluProThrCysGlnValIleGlnCysGluProLeuSerAlaProAspLe 267
|||||
879 GAACCAACCTGTCAAGTCAATGAGTCAAGCTCTATTCACGACCAAGATT 928
267 uGlyIleMetAsnCysSerHisProLeuAlaSerPheSerPheThrSera 284
|||||
929 GGGATCATGAACTGAGGCAATCCCTGGCAGCTTCAAGCTTACCTGTG 978
284 lAcSerThrPheIleCysSerGluGlyThrGluLeuIleGlyLysLys 300
|||||
979 CATGTAACCTTCATCTGCTCAGAGGAACTGAGTTAATTGGAGACAAAGAA 1028
301 ThrIleCysGluSerSerGlyIleTrpSerAsnProSerProIleCysGlu 317
|||||
1029 ACCATTGTGGAATCATCTGGAATCTGGTCAATCTAGTCAATATGTGCA 1078
317 nLysLeuAspLysSerPheSerMetIleLysGluGlyAspTrpAsnProL 334
|||||
1079 AAAATTGGACAAAGTTTCTCAATGATTAAAGAGGGTGATTAATACCCCC 1128
334 ePheIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
|||||
1129 TCTTCATTCCAGTGGCAGTCAATGTTACTCAATCTCTGTGGTGGCATTT 1178
351 IleIleTrpLeuAlaArgArgLeuLysGlyLysLysSerLysArgSe 367
|||||
1179 ATCATTTGGCTGGCAAGAGCATTTAAAAAAGGCAAAATCCAGAGAGAG 1228
367 rMetAsnAspProTrp 372
|||||
1229 TATGAAATGACCCATAT 1244

seq_name: /cgn2_2/gcdata/geneseq/geneseqn/NA1992.DAT:Q21184
seq_documentation_block:
ID Q21184 standard; DNA: 2350 BP.
AC Q21184:
XX
XX 21-MAY-1992 (first entry)
XX
XX DE Encodes T lymphocyte-specific Leu8 Antigen major form.
XX
XX KW Rapid immunoselection cloning technique: cell surface antigen;
XX homing receptor; antigen-presenting cells; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT CDS 50..1207
XX FT /tag= a
XX
XX PM M09201049-A.
XX
XX PD 23-JAN-1992.
XX
XX PF 15-JUL-1990; 90MO-US04986.
XX
XX PR 13-JUL-1990; 90US-0553759;
XX
XX PA (GEHO-) GEN HOSPITAL CORP.
XX
XX PI Seed B, Aruffo A, Amiot M,

```

XX WPI: 1992-056864/07.
 DR P-PSDB: R20815.
 XX
 PT New CD53 cell surface antigen and DNA encoding it - for
 PT immuno-therapy and diagnosis of haematopoietic neoplasms, etc.
 XX
 PS Example 14: Page 106; 160pp; English.
 XX
 CC Two cDNA clones encoding Leu8 determinants were isolated from a
 CC human T cell library using the rapid immunoselection cloning method
 CC (see e.g. Q21164 for description of method). The shorter insert
 CC (see Q22500) lacks 436 internal residues (i.e. nucleotides 1079 to
 CC 1514 of the longer insert). RNA blot hybridisation
 CC revealed a major transcript of 2.4kb in peripheral blood
 CC mononuclear cells, tonsillar B cells and the Jurkat and HSB-2
 CC leukaemic T cell lines. A minor transcript of 2.0kb was present in
 CC peripheral blood mononuclear cells and the Jurkat and HSB-2
 CC leukaemic T cell lines. The protein encoded by the larger insert
 CC is closely related to the murine Mel-14 homing receptor.
 XX
 S0 Sequence 2350 BP: 679 A; 519 C; 490 G; 662 T; 0 other:

alignment_scores:
 Quality: 2082.00 Length: 372
 Ratio: 5.627 Gaps: 0
 Percent Similarity: 99.462 Percent Identity: 98.656

alignment_block:
 US-09-119-209-2 x Q21184 ..

Align seg 1/1 to: Q21184 from: 1 to: 2350

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 |||||||
 89 ATGATATTTCCATGCAATGTCAGACACCAGAGGACTTATGGAACAT 138
 |||||||
 17 ePhelYsLeuTPGjLYTrPThrMetLeuCYsAspPheLeuAlaISH 34
 |||||||
 139 CTTCAGATTGTGGGGGTGACATGCTCTGTGTGATTTCTGGCCATC 188
 |||||||
 34 IsGLYThrCYsTrPrThrThrIstYrSerGlnLysProMeLAsnTP 50
 |||||||
 189 ATCGAACCCAGCTGCGACTTACCATTAATTCGAAACCAACCATGAC 238
 |||||||
 51 GlnAArgAlaAArgArGhPheCYsArGAspAsnYrThrAspLeuAlaL 67
 |||||||
 239 CAAAGGGCTAGAAAGATTCTGCCGAGCAATTAACAGATTAGTGCAT 288
 |||||||
 67 eGlnAsnLysAlaGluIleGLYTrLeuGluLysThrLeuProPheSer 84
 |||||||
 289 ACGAAACAGAGCGCAAAATGAGTATCTGGAGAAAGACTCTGCCCTTCAG 338
 |||||||
 84 rGSeTYrTYrPrIleGlyIleArGlysIleGlyLYleTrPrThrTP 100
 |||||||
 339 GTTCTTACTACGAGATAGGAATCCGGAACATAGCAACATATGACGCTG 388
 |||||||
 101 ValGlyThrAsnLysSerLeuThrGluAlaGluAsnTPGlyAspGI 117
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 389 GTGGGAACCCAACTCTCTCACTAGAAAGCAAGAACTGGGGAGATGG 438
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 117 YGluProAsnAsnLysLysAsnLysGluAspCysValGluIleTYrLe 134
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 439 TGAGCCCAACACAGAAAGAACAGAGAGCTGCGTGAGATCTATATCA 488
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 134 ySArGAsnLysAspAlaGlyLYsTrPAsnAspAspAlaCYsHIsLysLeu 150
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 489 ACAGAAACAAAGATGACGCAATGGAACGATGACGCCCTCCACAACAC 538
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 151 LysAlaAlaLeuCYsTYrThrAlaSerCYsGlnProTPSerCYsSerGI 167
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 539 AAGGAGCCCTCTGTACACAGCTTCTTCCAGCCCTGGTCATGACGTGG 588

167 yHISGLYGLYCysValGluIleLeAsnAsnHISThrCYsAsnCYsAspY 184
 |||||||
 589 CCATGAGAAATGTCGTAGAAATCATCAATATTAACACTGCACACTGTGATG 638
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 217 eSerPheSerSerGlnCYsAlaPheSerCYsSerGluGlyThrAsnLeu 234
 |||||||
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 839 GAACCAACCTGTCAAGTATCAGTGTGAGCCCTATTCAGCACACATTT 888
 |||||||
 267 uGlyIleMetAsnCYsSerHISProLeuAlaSerPheSerPheThSerA 284
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 367 rMetAsnAspProTYr 372
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 ID T14723 standard; cDNA; 2350 BP.
 XX
 AC T14723;
 XX
 DT 31-OCT-1996 (first entry)
 XX
 DE Human Leu8 antigen cDNA (major transcript).
 XX
 KW Cell surface antigen; cloning; immunoselection; immunotherapy;
 KW therapy; diagnosis; vector; COS; Leu9; T-lymphocyte; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key location/Qualifiers
 FT CDS 50..1207
 FT /*tag= a
 FT misc_feature 1079..1514

/*tag= b
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shorter cDNA clone"

US5506126-A.

09-APR-1996.

25-FEB-1988; 88US-0160416.

PR 01-DEC-1992; 92US-0983647.

PR 25-FEB-1988; 88US-0160416.

PR 13-JUL-1989; 89US-0379076.

PR 13-JUL-1990; 90US-0553759.

PR 18-OCT-1993; 93US-0139273.

(GENO) GEN HOSPITAL CORP.

Aruffo A. Seed B;

Cloning of cDNA encoding cell surface antigen - useful for isolation

of diagnostic and therapeutic proteins

Example 14; Column 71-74; 79pp; English.

2 cDNA clones encoding Leu8 determinants (R91442 and R91443) were isolated from a human T-cell library using a novel immunoselection cloning method. The longer insert (R14723) contained 2,350 residues, while the shorter lacked 436 internal residues but was otherwise identical. Dot blot hybridisation of a fragmented human T cell genome showed a pattern consistent with a single copy gene. A major transcript of 2.4 kb was present in peripheral blood mononuclear cells (PBMC), tonsillar B cells, and several lymphocytic cell lines, and a minor transcript of 2.0 kb in PBMC, Jurkat and HSB-2 leukemic T-cell lines. Leu8 antigens can be obt'd. for diagnostic and therapeutic use.

Sequence 2350 BP; 679 A; 520 C; 490 G; 661 T; 0 other;

alignment_scores:

Quality:	2082.00	Length:	372
Ratio:	5.627	Gaps:	0
Percent Similarity:	99.462	Percent Identity:	98.656

alignment_block:

US-09-119-209-2 x T14723

Align seg 1/1 to: T14723 from: 1 to: 2350

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89 ATGATATTTCATGCAATGTCAGACACCCAGAGGACTTATGAAACAT 138
  |||||||
17 ePheLysLeuTrpGlyTrpThrMetLeuCysCysAspPheLeuAlaHisH 34
  |||||||
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  |||||||
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  |||||||
189 ATGGAACCCAGCTGCGACTTACATTTATTCGAAAAACCCATGAACTGG 238
  |||||||
51 GlnAAGAlaArgArgPheCysArgAspAsnTyrThrAspLeuValAlaI 67
  |||||||
239 CAAAGGGCTAGAGATTCGCGAGACAAATTACACAGATTAGTTGCGCAT 288
  |||||||
67 eGlnAsnLysAlaGlnIleGluTyrLeuGluLysThrLeuProPheSera 84
  |||||||
289 ACAAAACAAGGGGGAATTTGATCTGTGGAGAAAGCTCTGCTTTCAAGTC 338
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84 rSerTyrTrpIleGlyIleArgLysIleGlyGlyIleTrpThrTrp 100
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  |||||||
389 GTGGAAACCAACAATCTCTCACTGAAAGCAGAGAACTGGGGAGATGG 438
  |||||||
117 yGluProAsnAsnLysLysAsnLysGluAspCysValGluIleTyrIle 134
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439 TGAGCCCAACAACAAGAACAGACAGAGAGTCCCTGGACATCTATATCA 488
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134 ySarArgAsnLysAspAlaGlyTyrTrpAsnAspAspAlaCysHisLysLeu 150
  |||||||
489 AGAGAAACAAGATGACAGCAAAATGAAAGATGAGACCTGCCACAACCTA 538
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151 LysAlaAlaLeuCysTyrThrAlaSerCysGlnProTrpSerCysSerG 167
  |||||||
539 AAGGACGCCCTCTGTATACACAGCTTCTTGCCAGCCCTGGTATGACGTG 588
  |||||||
167 yHisGlyGlyCysValGluIleIleAsnAsnHisThrCysAsnCysAspV 184
  |||||||
589 CCATGAGAGATGTGTAGAAATCATCATATATATACACCTGCAACTGTGATG 638
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201 GluAlaProGluLeuGlyThrMetAspCysThrHisProPheGlyAsnH 217
  |||||||
689 GAGGCCCAAGAGCTGGTATCATGATGACCTGATCTACTCTTTGGGAACTT 738
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  |||||||
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  |||||||
839 GAACCAACCTGTCAAGTATGATTCAGTGTGAGCTCTGTATGAGCACAATTT 888
  |||||||
267 uGlyIleMetAsnCysSerHisProLeuAlaSerPheSerPheTrpSera 284
  |||||||
889 GGGATATGACAGTGTAGCCATCCCTGGCCAGCTTACCTTTAACCTCTG 938
  |||||||
284 lAcysThrPheIleCysSerGlyGlyThrGluLeuIleGlyLysLysLys 300
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301 ThrIleCysGluSerSerGlyIleTrpSerAsnProSerProIleCysG 317
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989 ACCATTTGTAAATCATCTGGAATCTGTGTAATCTCAATCCATGCAATATGCA 1038
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317 nLysLeuAspLysSerPheSerMetIleLysGluGlyAspTyrAsnProL 334
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XX 07-JUN-1999 (first entry)
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XX Human Leu8 antigen cDNA.
XX
XX Leu8; cell surface antigen; human; T lymphocyte; cloning; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 50..1207
XX FT /*tag= a
XX
XX US5830731-A.
XX
XX PD 03-NOV-1998.
XX
XX PF 21-MAY-1997; 97US-0861205.
XX
XX PR 01-DEC-1992; 92US-0983647.
XX PR 25-FEB-1988; 88US-0160416.
XX PR 13-JUL-1989; 89US-0379076.
XX PR 13-JUL-1990; 90US-0553759.
XX PR 21-MAY-1997; 97US-0861205.
XX
XX PA (CEHO ) GEN HOSPITAL CORP.
XX
XX PI Acufco A, Seed B;
XX
XX DR WPI: 1998-609251/51.
XX DR P-PSDB: W80452.
XX
XX PT New cloning vector and polylinker - based on existing sequences for
XX PT efficient cloning and expression of mammalian cDNA(s), especially
XX PT human lymphocyte antigenic sequences
XX
XX PS Example 14; Column 67-70; 75pp; English.
XX
XX CC This nucleotide sequence comprises human Leu8 cDNA. The cDNA was
XX CC isolated from a human T lymphocyte cDNA library using a novel
XX CC method for cloning cDNAs from mammalian expression libraries. The
XX CC method is based on transient expression of an antigen in eukaryotic
XX CC cells and physical selection of cells expressing the antigen by
XX CC adhesion to an antibody-coated substrate. The method is useful for
XX CC the isolation and molecular cloning of any protein which can be
XX CC expressed and transported to the cell surface membrane of a
XX CC eukaryotic cell. It has been used to clone genes (see W63442-63)
XX CC encoding cell surface antigens from mammalian lymphocytes (see
XX CC W80440-55). The purified genes and proteins are useful for
XX CC immunodiagnostic and immunotherapeutic applications, including the
XX CC diagnosis and treatment of immune-mediated infections, diseases,
XX CC and disorders of animals, including humans. Leu8 (see W80452), a T
XX CC lymphocyte antigen, has been expressed in COS cells.
XX
XX SQ Sequence 2350 BP; 679 A; 521 C; 489 G; 661 T; 0 other;

alignment_scores:
Quality: 2082.00 Length: 372
Ratio: 5.627 Gaps: 0
Percent Similarity: 99.462 Percent Identity: 98.656

alignment_block:
US-09-119-209-2 x V63460 ..
Align seg 1/1 to: V63460 from: 1 to: 2350

1 MetIlePheProTPrLysCysGlnSerThrGlnArgAspLeuTrpAsnI 17
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89 AICATATTTTCATGCAATGTCAGACACACCAGAGGACTTATGCAACAT 138
17 ePheLysLeuTrpGlyTrpThrMetLeuLysCysAspPheLeuAlaIleH 34
|||||
139 CTTCAGATTGTGGGGGTGGCAATGCTCTGTGTGTGATTTCTCGGCATTC 188
34 IAGLYThrTyrCysTrpThrTyrHisTyrSerGlnLysProMetAsnTrp 50
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189 ATGGAACCGACTGCTGGACTTACCATTTATTCGMAAAACCCATGAACCTG 238
51 GlnArgAlaArgArgPheCysArgAspAsnTyrThrAspLeuValAlaI 67
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239 CAAAGCGCTAGAAAGATTCTGCCGACAAATTACACAGATTAGTGGCCAT 288
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|||||
289 ACAAAACAAGCGCGAAATTTGAGTATCTGGAGAAGACTGCTCTTCACATC 338
84 rGSerTyrTyrTrpIleArgLysIleGlyValTyrTrpTrp 100
|||||
339 GTTCTTACTACTGGATAGCAATCCGGAAGATAGGAGATATGACGTGG 388
101 ValGlyThrAsnLysSerLeuThrGluGluAlaGluAsnTrpGlyAsp 117
|||||
389 GTGGGAACCAACAANTCTCTCACTGAAAGACAGAACTGGGAGATGCG 438
117 yGluProAsnAsnLysLysAsnLysGluAspCysValGluIleTyrIle 134
|||||
439 TCAGCCCAACAACAAGAAACAGACAGACGTCGCGAGATCTATATCA 488
134 ySArgAsnLysAspAlaGlyLysTrpAsnAspAspAlaCysHisLysLeu 150
|||||
489 AGAGAAACAAGATGCGAGCAATGGACGATGACGCTGCCCAACAACTA 538
151 LysAlaAlaLeuCysTyrThrAlaSerCysGlnProTrpSerCysSer 167
|||||
539 AAGGACGCCCTCTGTTACACACCTTCTTCCAGCCCTGTCATGCACTGG 588
167 yHisGlyGluCysValGluIleLeuAsnAsnHisThrCysAsnCysAsp 184
|||||
589 CCATGGAGATGCTGTAGAATCATCAATTAATACACTTCAACTGTGATG 638
184 aIGLYTyrTyrGlyProGlnCysGlnLeuValIleGlnCysGluProLeu 200
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639 TGGGTTACTATGGGCCCCAGTGTCAAGTTGTGATTCAGTGAAGCTTTGG 688
201 GluAlaProGluLeuGlyThrMetAspCysThrHisProPheGlyAsn 217
|||||
689 GAGGCCCCAGACTGGTATGCACTGCACTACTCACTCTTTGGAAACAT 738
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267 uGlyIleMetAsnCysSerHisProLeuAlaSerPheSerPheThrSer 284
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284 IAcysThrPheIleCysSerGlnGlyThrGluLeuIleGlyLysLys 300
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939 CATGTACTTCAATCTGCTCAGAAAGAACTGAGTTAATTTGGAAAGAA 988
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1139 ATCATTTGGCTGGCAAGAGATTAAAAAGCAAGAAATCCAGAGAAAG 1188
367 rMetAsnAspProTyr 372
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AC V81217;
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XX 10-MAY-1999 (first entry)
XX
XX Human Leu8 antigen cDNA.
DE
XX Leu8: cell surface antigen; human; T lymphocyte; cDNA library;
XX ss.
XX Homo sapiens.
OS
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XX
XX 15-DEC-1998.
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XX 07-JUN-1995; 95US-0485447.
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XX 01-DEC-1992; 92US-0983647.
XX 25-FEB-1988; 88US-0160416.
XX 13-JUL-1989; 89US-0379076.
XX 23-MAR-1990; 90US-0488809.
XX 13-JUL-1990; 90US-0553759.
XX 07-JUN-1995; 95US-0485447.
XX
XX (GENO ) GEN HOSPITAL CORP.
XX
XX Allen J, Amiot M, Aruffo A, Camerini D, Lauffer L;
XX Oquendo C, Seed B, Simmons D, Stamenkovic I, Stengelin S;
XX WPI: 1999-069813/06.
XX P-PSDB: W86199.
XX
XX Example 14; Column 67-70; 79pp; English.
XX
XX This nucleotide sequence comprises human Leu8 cDNA. The cDNA was
XX isolated from a human T lymphocyte cDNA library using a novel
XX method for cloning cDNAs from mammalian expression libraries. The
XX method is based on transient expression of an antigen in eukaryotic
XX cells and physical selection of cells expressing the antigen by
XX adhesion to an antibody-coated substrate. The method is useful for
XX the isolation and molecular cloning of any protein which can be
XX expressed and transported to the cell surface membrane of a

```

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CC eukaryotic cell. It has been used to clone genes (see V81198-220)
CC encoding cell surface antigens such as CD4, CD1b, CD1c, CD2, CD6,
CC CD7, CD13, CD14, CD16, CD19, CD20, CD22, CD26, CD27, CD28, CD31,
CC CDw32a, CDw32b, CD33, CD34, CD36, CD37, CD38, CD39, CD40, CD43,
CC CD44, CD55, ICAM, LFA-3, FCRIa, FCRIb, T11sa and Leu8 (see
CC W86188-62, W89151-52 and W88451). CD40 cDNA (see V81198) is
CC specifically claimed. Leu8, a T lymphocyte antigen, has been
CC expressed in COS cells.
XX
XX Sequence 2350 BP; 679 A; 521 C; 489 G; 661 T; 0 other;

alignment_scores:
Quality: 2082.00 Length: 372
Ratio: 5.627 Gaps: 0
Percent Similarity: 99.462 Percent Identity: 98.656

alignment_block:
US-09-119-209-2 x V81217 ..
Align seg 1/1 to: V81217 from: 1 to: 2350

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89 ATGATATTTCATCGAATGGAATGTGACAGACCCAGAGGACTTATGAAACAT 138
17 ePheLysLeuTPrGlyTPrThrMetLeuCysCysAspPheLeuAlaHisH 34
139 CTTCAAGTTGTGGGGGTGGACAAATGCTCTGTGATTCTTCTGCGACATTC 188
34 lSGlyThrTyrCysTPrThrTyrHisTyrSerGluLysProMetAsnTPr 50
189 ATGGAACCGAGCTGCTGAGATTACCATTTATTCGAAAAACCCATGAACCTG 238
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339 GTTCTTACTACTGATGATGAAATCCGAGAGATGAGAGAAATGACAGCTGG 388
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117 yGluProAsnAsnLysLysAsnLysGluAspCysValGluIleTPrIle 134
439 TGAGCCCAACAAAGAAAGAAACAAAGAGAGAGCTGGGAGATCATATATCA 488
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151 LysAlaAlaLeuCysTyrThrAlaSerCysGlnProTPrSerCysSerG1 167
539 AAGGAGGCGCTCTGTTCACAGCTTCTTGGCAGCCCTGGCATGAGTGG 588
167 yHisGlyLysCysValGluIleIleAsnAsnHisThrCysAsnCysAspY 184
589 CCATGAGACAATGTGTAGAAATCATCATATATTCACCTGCAACTGTGATG 638
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639 TGGGCTACTATGGGCCCCAGCTGACGTTGTGATCATGAGTGCACCTTTG 688
201 GluAlaProGluLeuGlyThrMetAspCysThrHisProPheGlyAsnPh 217
689 GAGGCCCAAGAGCTGGGTACCATGAGACTGTACTCTTTGGAAACTT 738

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      |||||||
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1089 TCTTTCATTCCAGTGCAGTCATGCTTACATCTCTGGCTGGCATTTT 1138
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seq_documentation_block:

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AC Q38839:

DT 17-AUG-1993 (first entry)

DE Sequence of LAM-1 cDNA.

XX Leukocyte adhesion molecule-1, lymphocyte-associated molecule-1;

KW LAM-1; ss.

OS Homo sapiens.

FT key Location/Qualifiers

FT CDS 53..1210

FT /*tag= a

PN MO9306835-A.

PD 15-APR-1993.

PF 05-OCT-1992; 92WO-2008467.

PR 03-OCT-1991; 91US-0770608.

PA (DAND) DANA FARBER CANCER INST INC.

PI Tedder TF, Spertini OG;

```

DR WPI: 1993-134119/16.
DR P-PSDB: R34197.
PT Detection of inflammation or disease site - by using labelled
PT Leukocyte adhesion molecule-1 - treats leukocyte-mobilising
PT conditions, auto-immune disorders, cancer etc.
PS Disclosure: Fig 2; 44pp; English.
XX
CC cDNA encoding the LAM-1 protein was isolated from a human tonsil
CC cDNA library (ATCC 37546). The mature LAM-1 protein has an
CC extracellular region of about 294 amino acids containing 7 potential
CC N-linked carbohydrate attachment sites. LAM-1 has a cytoplasmic tail
CC of 17 amino acids containing 8 basic and 1 acidic residues. The
CC processed LAM-1 protein has a Mr of at least 50,000. LAM-1 combines
CC domains homologous to domains found in three distinct families of
CC molecules: animal lectins, growth factors, and C3/C4 binding proteins.
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SQ Sequence 2330 BP; 661 A; 527 C; 482 G; 660 T; 0 other:

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Ratio:	5.611	Gaps:	0
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Align seg 1/1 to: Q38839 from: 1 to: 2330

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: Sequence 1, Application US/08481803
: Patent No. 5679346
: GENERAL INFORMATION:
: APPLICANT: Tedder, Thomas F. and Olivier G. Sperlnt
: TITLE OF INVENTION: MONOCLONAL ANTIBODY TO LYMPHOCYTE-ASSOCIATED CELL
: NUMBER OF SEQUENCES: 1
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FISH & NEAVE
: STREET: 1251 Avenue of the Americas
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10020
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/481,803
: FILING DATE:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/215,366
: FILING DATE: 21-MAR-1994
: APPLICATION NUMBER: US 07/720,602
: FILING DATE: 25-JUN-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/313,109
: FILING DATE: 21-FEB-1989
: ATTORNEY/AGENT INFORMATION:
: NAME: James F. Haley, Jr.
: REGISTRATION NUMBER: 27,794
: REFERENCE/DOCKET NUMBER: CG-101 CON
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 596-9000
: TELEFAX: (212) 596-9090
: TELEX:
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2330 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 53..1210
: US-08-481-803-1

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 Percent Similarity: 99.462 Percent Identity: 98.118

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Align seg 1/1 to: US-08-481-803-1 from: 1 to: 2330

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: Sequence 1, Application US/08215366A
: Patent No. 576775
: GENERAL INFORMATION:
: APPLICANT: Tedder, Thomas F. and Olivier G. SperlinI
: TITLE OF INVENTION: MONOCLONAL ANTIBODY TO LYMPHOCYNE-ASSOCIATED
: NUMBER OF SEQUENCES: 1
: CORRESPONDENCE ADDRESS:
: ADDRESS: WHITE & CASE
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/215,366A
: FILING DATE: 21-MAR-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/720,602
: FILING DATE: 25-JUN-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/313,109
: FILING DATE: 21-FEB-1989
: ATTORNEY/AGENT INFORMATION:
: NAME: Neils T. Lipsett
: REGISTRATION NUMBER: 25,888
: REFERENCE/DOCKET NUMBER: 1110684-0005
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 819-8582
: TELEFAX: (212) 354-8113
: TELEX:
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2330 base pairs
: TYPE: nucleic acid

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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEITICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
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US-08-215-366A-1

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  : Patent No. 5808025
  : GENERAL INFORMATION:
  : APPLICANT: Tedder, Thomas F.
  : TITLE OF INVENTION: KANSAS, Geoffrey S.
  : TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
  : NUMBER OF SEQUENCES: 28
  : CORRESPONDENCE ADDRESS:
  : ADDRESSEE: FISH & NEAVE
  : STREET: 1251 Avenue of the Americas
  : CITY: New York
  : STATE: New York
  : COUNTRY: USA
  : ZIP: 10020
  : COMPUTER READABLE FORM:
  : MEDIUM TYPE: floppy disk
  : COMPUTER: IBM PC compatible
  : OPERATING SYSTEM: PC-DOS/MS-DOS
  : SOFTWARE: Patentin Release #1.0, Version #1.30
  : CURRENT APPLICATION DATA:
  : APPLICATION NUMBER: US/08/340,539A
  : FILING DATE: 16-NOV-1994
  : CLASSIFICATION: 514
  : PRIOR APPLICATION DATA:
  : APPLICATION NUMBER: US 08/008,459
  : FILING DATE: 25-JAN-1993
  : ATTORNEY/AGENT INFORMATION:
  : NAME: Gunnison, Jane
  : REGISTRATION NUMBER: 38,479

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: REFERENCE/DOCKET NUMBER: CG-104 CON
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-596-9000
: TELEFAX: 212-596-9090
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2330 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 53..1207
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US-09-119-209-2 x US-08-340-539A-1 ..
Align seg 1/1 to: US-08-340-539A-1 from: 1 to: 2330

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592 CCATGGAAGATGTGTAGAAATCATCAATATATACACTGCAACTGTGAT 641
184 aLgTyTrpGlyProGlnCysGlnLeuValIleGlnCysGluProLeu 200
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642 TGGGCTACTATGGGCCCGCCAGTGTGATTTGATTCAGTGTGACCCCTT 691
201 GluAlaProGluLeuGlyThrMetAspCysThrHisProPheGlyAsn 217
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692 GAGGCCCGAGAGCTGGGTACATGACATCTACTACACCTTTGGAAACT 741
217 eSerPheSerSerGlnCysAlaPheSerCysSerGluGlyThrAsnLeu 234
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742 CAAGCTCAACCTCAGAGTGTGCTTCAAGTGTCTGTGAGGAAACAAC 791
234 hGlyIleGluGluThrThrCysGlyProPheGlyAsnTrpSerSerPro 250
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792 CTGGATTTGAAGAAACACACCTGTGAACCATTTGGAACCTGTCACT 841
251 GluProThrCysGlnValIleGlnCysGluProLeuSerAlaProAsp 267
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842 GAACCAACCTGTCAAGTATGATTCAGTGTGAGCTCTATTCAGCACCA 891
267 uGlyIleMetAsnCysSerHisProLeuAlaSerPheSerPheThrSer 284
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892 GGGATCATGAACCTGTAGGCAATCCCTGGCCAGCTTCACCTTACTCT 941
284 lAcysThrPheIleCysSerGluGlyThrGluLeuIleGlyLysLys 300
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942 CATGTACCTTCATCTGCTCAGAAAGAACTGATTAATGGAAAGAAA 991
301 ThrIleCysGluSerSerGlyTrpSerAsnProSerProIleCysG 317
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317 nLysLeuAspLysSerPheSerMetIleLysGluGlyAspTyrrAsnPro 334
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334 eUpheIleProValAlaValMetValThrAlaPheSerGlyLeuAla 350
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1092 TCTTCATTTCCAGTGGCAGATCATGTTACTGCAATCTCTGGTTCG 1141
351 IleIleTrpLeuAlaArgArgLeuLysLysGlyLysLysSerLysArg 367
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1142 ATCATTTGGCTGTCAGAGAGATTAAGAAAGCAAGAAATCCAGAGAG 1191
367 rMetAsnAspProTyrr 372
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1192 TATGAATGACCATAT 1207

seq_name: /cgn2_6/prodata/2/ina/5B-COMB.seq:US-08-461-592B-1
seq_documentation_block:
: Sequence 1, Application US/08461592B
: Patent No. 5834425
: GENERAL INFORMATION:
: APPLICANT: Tedder, Thomas F.
: APPLICANT: Kansas, Geoffrey S.
: TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
: TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Weingarten, SchurJin, Gagnebin & Hayes
: STREET: Ten Post Office Square
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/461,592B
: FILING DATE:
: CLASSIFICATION: 514
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/340,539
FILING DATE: 16-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: James F. Hailey, Jr.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: CG-104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2330 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 53..1210
US-08-461-592B-1

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Ratio: 5.611          Gaps: 0
Percent Similarity: 99.462      Percent Identity: 98.118

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292 ACAAACAAGCGGGAATTGAGTATCTGGAGACAAGCTCTGCTTTCATC 341
84 rGSerTyrTrpTrpIleGlyIleArgLysIleGlyGlyIleTrpThrTrp 100
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117 yGluProAsnAsnLysLysAsnLysGluAspCysValGluIleTyrIle 134
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442 TGAGCCCAACAACAAGAAAGACAGAGGAGCTGGCTGGAATCTATATCA 491
134 ySArgAsnLysAspAlaGlyLysTrpAsnAspAspAlaCysHisLysLeu 150
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151 LysAlaAlaLeuCysTyrThrAlaSerCysGlnProTrpSerCysSerG 167
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167 yHisGlyGluCysValGluIleIleAsnAsnHisThrCysAsnCysAsp 184
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592 CCATGAGATGATGTAGAAATCATCAATTAATTACACCGCAACTGTGATG 641
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351 IleIleTrpLeuAlaArgArgLeuLysLysGlyLysSerLysArgSe 367
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1192 TATGATGACCCATAT 1207

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PATENT NO. 5514582
APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A.
TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 43
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,670
FILING DATE: 21-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 986,931
FILING DATE: 08-DEC-1992
APPLICATION NUMBER: 808,122
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; FILING DATE: 16-DEC-1991
; APPLICATION NUMBER: 440,625
; FILING DATE: 22-NOV-1989
; APPLICATION NUMBER: 315,015
; FILING DATE: 23-FEB-1989
; SEQ ID NO:1:
; LENGTH: 1829
5514582-1

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Ratio: 5.607 Gaps: 1
Percent Similarity: 98.925 Percent Identity: 98.656

alignment_block:
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17 ePheIysLeuTrpGlyTrpThrMetLeuCyScyAspPheLeuAlaHis 34
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179 CTTCAGATTGTGGGGGTGGACATGCTCTGTGTGATTTCTTGCGCACATC 228
34 IsgIlyThrTyrcysTrpThrTyrrHisTyrSerGluIysProMetAsnTrp 50
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229 ATGGAACCTACTGCTGACTTACCATTTATTTGAAAACCCATGAACGTGG 278
51 GlnArgAlaArgArgPheCysArgAspAsnTyrrThrAspLeuValAlaIli 67
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84 rGserTyrrTyrrTrpIleGlyIleArgLysIleGlyIleTyrrTrpTrp 100
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284 IacysThrPheIleCysSerGluGlyThrGluLeuIleGlyLysLysLys 300
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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-513-278-3
seq_documentation_block:
: Sequence 3, Application US/08513278
: Patent No. 5840844
:
: GENERAL INFORMATION:
: APPLICANT: LASKI, LAURENCE A.
: APPLICANT: STACHELL, SCOTT E.
: APPLICANT: ROSEN, STEVEN D.
: APPLICANT: SINGER, MARK S.
: APPLICANT: YEDNOCK, TED A.
:
: TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
:
: NUMBER OF SEQUENCES: 6
:
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/513,278
: FILING DATE: 10-AUG-1995
: CLASSIFICATION: 5530
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: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/059027
: FILING DATE: 06-MAY-1993
: APPLICATION NUMBER: 07/786149
: FILING DATE: 31-OCT-1991
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; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/315015
; FILING DATE: 23-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET INFORMATION: 565D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2214 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; US-08-513-278-3
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    Ratio: 4.988          Gaps: 0
    Percent Similarity: 88.978    Percent Identity: 76.075
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alignment block:

US-09-119-209-2 x US-08-513-278-3 ..

Align seg 1/1 to: US-08-513-278-3 from: 1 to: 2214

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67 eGlnAsnLysAlaGluIleGlyTrrLeuGlyLysThrLeuProPheSerA 84
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101 ValGlyThrAsnLysSerLeuThrGlnGluAlaGluAsnTrrpGlyAspG 117
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seq_documentation_block:
; Patent No. 5514582
; APPLICANT: CAPON, DANIEL J.; TASKY, LAURENCE A.
; TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
; IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 43
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US-08/185,670
; FILING DATE: 21-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 986,931
; FILING DATE: 08-DEC-1992
; APPLICATION NUMBER: 808,122
; FILING DATE: 16-DEC-1991
; APPLICATION NUMBER: 440,625
; FILING DATE: 22-NOV-1989
; APPLICATION NUMBER: 315,015
; FILING DATE: 23-FEB-1989
; SEQ ID NO: 3
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5514582-3
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alignment_scores:

Quality: 1651.00 Length: 372
 Ratio: 4.988 Gaps: 0
 Percent Similarity: 88.978 Percent Identity: 76.075

alignment_block:

us-09-119-209-2 x 5514582-3 ..

Align seg 1/1 to: 5514582-3 from: 1 to: 2214

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456 GGAGCCCAACAAAGAAAGTCCAAAGGAGAGCTGTGGAGATCTATATCA 505
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506 AGAGGAGACGAGACTCTGGAAATGGAATGGAACGATGACCCCTGTACAAAGCA 555
151 LysAlaAlaLeuCysTYrThrAlaSerCysGlnProTrrPserCysSerG1 167
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556 AAGGCAGCTCTGTCTACACAGCCCTTGGCCAGGAGGTCTTGCATATGG 605
167 yH1sGIYGLuLysValGluIleIleAsnAsnH1sThrCysAsnCyAspV 184
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201 GlnAlaProGluLeuGlyThrMetAspCysTrH1sProPheGlyAsnPh 217
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217 eSerPheSerSerGlnCysAlaPheSerCysSerGluGlyThrAsnLeuT 234
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856 GAGCCAAATCTGCCAAGTGTCCAGTGTGAGCCTTGGAGGCCCTGAGATT 905
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956 ACTGTGCTTTCAACGTCTGTGAGGAGAGAGACTTCTTGGACATGCACAAA 1005
301 ThrIleCysGluSerSerGlyIleTrPserAsnProSerProIleCysG1 317
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1006 ACACAGTGTGGAGATCTGGAAMCTGTCAATCTCCAGAGCCCAATCTGCCA 1055
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seq_documentation_block:
; Sequence 3, Application US/08110158
; Patent No. 5605821
; GENERAL INFORMATION:
; APPLICANT: Mcever, Rodger P.
; APPLICANT: Pan, Junliang
; TITLE OF INVENTION: Expression Control Sequences of the
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; City: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,158
; FILING DATE: 19930820
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/320,408
; FILING DATE: 08-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3142 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

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LOCATION: 2833..2838
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: OTHER INFORMATION: signals"
: FEATURE:
: NAME/KEY: polyA-signal
: LOCATION: 3124..3130
: OTHER INFORMATION: /note= "potential polyadenylation
: OTHER INFORMATION: signal"
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169 ATCATTTACGACACAAAGCATATCTCATGGAATATTTCCCGTAAATCTTC 218
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58 ArgAspAsnTYTrHrAspLeuValAlaIleGlnAsnLysAlaGluIleG 74
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519 GCCTCTCTGCCAGACATGCTCTGACAGCAACAGACAGACTGCTTGACGC 568
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174 eIleAsnAsnHnIstYrCysAsnCysAspValGlyTYrTYrGlyProGln 191
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719 CTTCCACTGCACTGACGGGTACCAAGTAAATGGGCCCAACAGACTGGAA 768
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seq_documentation_block:
: Sequence 2, Application US/08365470
: Patent No. 5632991
: GENERAL INFORMATION:
: APPLICANT: Gimbroe, Jr., Michael A.
: TITLE OF INVENTION: Antibodies Specific For E-selectin And The Uses
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX
: STREET: 1100 New York Ave., NW
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/365.470
: FILING DATE: herewith
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/102,510
: FILING DATE: 05-AUG-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/850,802
: FILING DATE: 13-MAR-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Markowicz, Karen R.
: REGISTRATION NUMBER: 36,351
: REFERENCE/DOCKET NUMBER: 0627.1350003
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-2540
: TELEFAX: 202-371-2540
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1833 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: nucleic acid
: LOCATION: 1-1833
: OTHER INFORMATION: /label = nucleic acid
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55 gPhcCysArgAspAsnTyrThrAspLeuAlaAlaIleGlnAsnLysAlaG 72
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164 AGATTGAGTACCTTAACCTCATATGAGCTATTCACCAAGTTATTACTGG 213
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89 IleGlyIleArgGlyIleGlyGlyIleTyrPheTyrValGlyThrAsnLys 105
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: Sequence 18, Application US/09209668A
: Patent No. 6114517
: GENERAL INFORMATION:
: APPLICANT: Monia, Brett P.
: APPLICANT: Xu, Xiaoxing S.
: TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
: TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
: FILE REFERENCE: ISPH-0336
: CURRENT APPLICATION NUMBER: US/09/209,668A
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 18
: LENGTH: 3834
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (117)..(1949)
: PUBLICATION INFORMATION:
: DATABASE ACCESSION NUMBER: M24736/genbank
: DATABASE ENTRY DATE: 1994-11-07
US-09-209-668-18

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 Percent Similarity: 79.570 Percent Identity: 51.971

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55 gPhcCysArgAspAsnTyrThrAspLeuAlaAlaIleGlnAsnLysAlaG 72
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230 TTAATGTACAGCAAGGTACACACCTGTTGCATTTCAAAACCAAGAAG 279
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280 AGATTGAGTACCTTAACCTCATATGAGCTATTCACCAAGTATTATACGG 329
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89 IleGlyIleArgGlyIleGlyGlyIleTyrPheTyrValGlyThrAsnLys 105
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330 ATTGGAATCAGAAAAGTCAACAATGTGTGTGTGTGTGTGTGTGTGTGT 379
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105 sSerLeuThrGluGluAlaGluAsnTyrPylAspGlyLysLysLysLysL 122
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
380 ACCTTGACAGAAAGAACCCAGAACCTGGCTCCAGTATACCAACCAATA 429
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
122 yslYsAsnLysGluAspCysValGluIleTyrIleLysArgAsnLysAsp 138
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
430 GGCAAAAAGATGAGAGCTGGGAGATCTACATCAGAGAGAGAAAAGAT 479
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
139 AlaGlyLysTrpAsnAspAspAlaCysHisLysLeuLysAlaAlaLeuCy 155
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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: SEQUENCE CHARACTERISTICS:
: LENGTH: 3858
: TYPE: Nucleic Acid
: STRANDEDNESS: Single
: TOPOLOGY: Linear
: ANTI-SENSE: No
US-08-344-155C-98

alignment_scores:
    Quality: 862.00      Length: 279
    Ratio: 3.883         Gaps: 0
    Percent Similarity: 79.570      Percent Identity: 51.971

alignment_block:
US-09-119-209-2 x US-08-344-155C-98  ..

Align seg 1/1 to: US-08-344-155C-98 from: 1 to: 3858

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254  TTATTGTGACGAAGAAGTACACACACCGTGTTGCATTCCAAACAAAG  303
72  LuIleGluTyrLeuGluLysThrLeuProPheSerArgSerTyrTyrTrp  88
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
304  AGATTGAGTACCTAAACCTCATATGTAGCTATTCACCAAGTATTACTG  353
89  IleGlyIleArgLysIleGlyGlyIleTrpThrValGlyHisAsnLys  105
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
354  ATTGGAAATCAGAAAAGTCACAAACATGTGTGGGTGGTGAAGAACCA  403
105  sSerLeuThrGluGluAlaGluAsnTrpGlyAspGlyGluProAsnAsn  122
404  ACCTGTGACGAAGAAGCCACGAACCTGGCGCTCCAGCTGAACCCACAT  453
122  ySLysAsnLysGluAspCysValGluIleTyrIleLysArgAsnLysAsp  138
454  GGCAGAAAAGATGAGACCTGCGTGGAGATCTTCACTCAAGAGAAAAGAT  503
139  AlaGlyLysTrpAsnAspAspAlaCysHisLysLysLeuLysAlaAla  155
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
504  GTGGCGCATGTGGAAATGATGAGAGCGTCACACGAAGAAGAAGCTTGC  553
155  sTyrTrpAlaSerCysGlnProTrpSerCysSerGlyHisGlyLysCysV  172
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
554  CTACACAGCTGCGCTGTACCAATACATCTCGCAGTGGCCAGCGTGAATG  603
172  aIGluIleLeaAsnAsnHisThrCysAsnCysAspValGlyTyrTyrGly  188
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
604  TAGAAGACCTCATATATTATTAACCTTGCAGTGTGACCCCGCTTCACTG  653
189  ProGlnCysGlnLeuValIleGlnCysGluProLeuGluAlaProGluLe  205
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
654  CTCAGAGTGTGACCAATTTGTAAACTGTACACCCCTGTGAATCCCTGAC  703
205  uGlyIleMetLysCysTrpHisTrpPheGlyAsnPheSerPheSerGerg  222
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
704  TGGAAAGCCTGGTTGGACATCCACCCAGTGGAAACTTCAAGCTACAACTT  753
222  LncYsAlaPheSerCysSerGluGlyThrAsnLeuThrGlyIleGluGlu  238
CCTGCTCTATACCTGTGATAGGAGTACTCTGCGCAACAGACAGATGGAA  803
239  ThrThrCysGlyProPheGlyAsnTrpSerSerProGluProThrCysGly  255
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
804  ATGCAGCTATGTCCTCTGGAGATGAGTGCCTCATTTCCACCCCTGCAAA  853
255  nValIleGlnGluProLeuSerAlaProAspLeuGlyIleMetAsnC  272
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272 ysserHisProleuAlaserPheSerPheThrSerAlaCysThrPheIle 288
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904 GTTCCAAAACCTGGAGCTTCCCATGGACACAAACCTGTACATTGAC 953
289 CysSerGluGlyThrGluLeuIleGlyLysLysLysThrIleCysGlu 305
      ::::: ::::: ::::: ::::: ::::: :::::
954 TGTGAAGAAGGATTTGAACTAATGGAGGCCAGAGCCTTCAGTGTACCTC 1003
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seq_documentation_block:
; Patent No. 5217870
; APPLICANT: HESSION, CATHERINE A.; LOBB, ROY R.; GOELZ, SUSAN E.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST CDX
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/345,151
; FILING DATE: 28-APR-1989
; SEQ ID NO:1
; LENGTH: 3863
5217870-1

alignment_scores:
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US-09-119-209-2 x 5217870-1 ..

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55 gPheCysArgAspAsnTYrThrAspLeuValAlaIleGlnAsnLysAlaG 72
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254 TTATTTGTGCAAGGTACACACACCTGTTGCAATTCAAAACAAAGAAG 303
72 IuIleGluTrpLeuGluLysTrpLeuProPheSerArgSerTYrTYrTrp 88
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304 AGATTGAGTACCTAAACCTCATATTGAGCTATTTCACCAAGTTATTACTCG 353
89 IlegIyIleArgLysIleGlyIleTrpTrpIleValAlaGlyThrAsnLys 105
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105 sSerLeuTrpGluGluAlaGluAsnTrpGluLysPglLysGluProAsnL 122
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122 ySLysAsnLysGluAspCysValGluIleTYrIleLysArgAsnLysAsp 138
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454 GGCAAAAGATGAGACGCTGCGTGAAGATCTACATCAAGAGAAAAAGAT 503
139 AlaGlyLysTrpAsnAspAspAlaCysHisLysLeuLysAlaAlaLeuCy 155
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504 GTGGCCATGTGAATGATGAGAGGTGCACAGAAAGAACCTTGCCCTATGC 553
155 sTYrThrAlaSerCysGlnProTrpSerCysSerGlyHisGlyLysCysV 172
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554 CTACACAGCTGCTGTACCAATACATCTGCGAGTGGCCAGGTTGAATGTG 603
172 aIGluIleIleAsnAsnHisThrCysAsnCysAspValGlyTYrTYrGly 188
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654 CTGAATGTGAGCAATTTGGAACCTGTACAGCCCTGGAAATCCCTTAGCA 703
205 uGlyTrpMetAspCysThrHisProPheGlyAsnPheSerPheSerSerc 222
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704 TGGAGCCTGTGTTTGCAGTCACCCACTGGGAACCTTCAGCTACAAATTCCT 753
222 IncSylAlaPheSerCysSerGluGlyThrAsnLeuThrGlyIleGlu 238
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754 CTGCTCTATCAGCTGTGATAGGGTTACCTGCCAAGACAGACATGAGACCC 803
239 ThrThrCysGlyProPheGlyAsnTrpSerSerProGluProThrCysG 255
      ::::: ::::: ::::: ::::: ::::: :::::
804 ATGCACTGTATGCTCTCTGGAGATGAGTGTCTATTTCAGCTGACAA 853
255 nValIleGlnCysGluProLeuSerAlaProAspLeuGlyIleMetAsn 272
      ::::: ::::: ::::: ::::: ::::: :::::
854 TGTGTTGAGTGTGATGCTGTGACAAATCCAGCCATGGGTTGCTGGAAAT 903
272 ysserHisProleuAlaserPheSerPheThrSerAlaCysThrPheIle 288
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Date: Jan 13, 2001 3:39 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000
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Search information block:

Query: US-09-119-209-2
Query length: 372
Database: Pending_Patents_NA*
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1. Application US/09119209
GENERAL INFORMATION:
APPLICANT: LASKY, LAURENCE A.
APPLICANT: STACHELL, SCOTT E.
APPLICANT: ROSEN, STEVEN D.
APPLICANT: SINGER, MARK S.
APPLICANT: YENDOCK, TED A.
TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/119,209
FILING DATE: 20-Jul-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/513278
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/059027
FILING DATE: 6-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/786149
FILING DATE: 31-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/315015
FILING DATE: 23-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0565D1C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2259 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-119-209-1
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979 CATGTACCTTATCTCTGACAGAACTGAGTTAATTTGGGAAGAAAGAAA 1028
301 ThrIleCysGluSerSerGlyIleTrpSerAsnProSerProIleCysG 317

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1029 ACCATTGTGATCATCTGGAATCTGTCAAACTCTAGTCCATATATGTCA 1078
317 dLysLeuAspLysSerPheSerMetIleLysGluGlyAspTyrAsnPOL 334
1079 AAAATTGGACAAAGTTTCTCATGTATTAAAGAGGGTGATTATTAACCCCC 1128
334 euPheIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
1129 TCTTATTCAGAGTGGCACTCATGTTACTGATCTCTGTGGTTGGCATTT 1178
351 lleIleThrPheLeuAlaArgArgLeuLysGlyLysLysSerLysArgSe 367
1179 ATCATTTGCTGTGGCAAGAGATTTAAAAAGCAAGAAATCACAAGAGAAG 1228
367 rMetAsnAspProTyr 372
1229 TATGATGACCCATAT 1244

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seq_name: /cgn2.6/prodata/2/pna/US090_COMB.seq:US-09-023-655-1154

seq_documentation block:

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: Sequence 1154, Application US/09023655
: GENERAL INFORMATION:
: APPLICANT: Cocks, Benjamin G.
: APPLICANT: Susan G. Stuart
: APPLICANT: Jeffrey J. Seilhamer
: TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
: NUMBER OF SEQUENCES: 1508
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
: STREET: 3174 PORTER DRIVE
: CITY: PALO ALTO
: STATE: CALIFORNIA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/023.655
: FILING DATE: HERewith
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Zeller, Karen J.
: REGISTRATION NUMBER: 37, 071
: REFERENCE/DOCKET NUMBER: PA-0001 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (650) 855-0555
: TELEFAX: (650) 845-4166
: INFORMATION FOR SEQ ID NO: 1154:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2354 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: GENBANK
: CLONE: 9187182
: US-09-023-655-1154

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alignment_scores:

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Quality: 2094.00      Length: 372
Ratio: 5.644          Gaps: 0
Percent Similarity: 99.731  Percent Identity: 99.194

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alignment_block:
US-09-119-209-2 x US-09-023-655-1154 ..

Align seg 1/1 to: US-09-023-655-1154 from: 1 to: 2354

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1 MetIlePheProTrrPlyScySglInSerThrGlnAtrGAspLeuTrrPAsnI 17
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116 ATGATAATTTCCATGTGAAATGTGAGAGCACCCAGAGGACTTATGTGAACAT 165
17 ePheLysLeuTrrPglYTrPThrMetLeuCyScyAspPheLeuAlaHisH 34
  |||
166 CTTCACAGTTGTGGGGGTGGACAAATGCTCTGTGTGTATTTCTGGCACATC 215
34 IsGlyThrTyrcysTrrPThrThrsTySercGluLysProMetAsnTrrP 50
  |||
216 ATGGAACGACGACTGCTGACTTACCATTTATTCGAATAAACCCATGAACTGG 265
51 GlnAtrGAlaAtrGArpPheCysAtrGAspAsnTyrrThrAspLeuValAla 67
  |||
266 CAACGGCGTAGAAGATTTCTGCCGAGACAATTCACAGATTAGTTGCCAT 315
67 eGlnAsnLysAlaGluIleGlyTrLeuGluLysThrLeuProPheSerA 84
  |||
316 ACAAAACAAGCGGGAATTTGAGTATCTGGAGAAAGACTTGCCTTTTCAGTC 365
84 rGserTyrrTyrrPrlIleGlyIleAtrGlysIleGlyGlyTrIleTrrPThr 100
  |||
366 GTTCTTACTACTGATAGSAAATCCGGAACATGAGAGAAATATGAGACTGG 415
101 ValGlyThrAsnLysSerLeuThrGluAlaGluAsnTrrPglYAspSgl 117
  |||
416 GTGGAAACCAACAATCTCTTACTGAAAGCAGACAACCTGGGGAGATG 465
117 yGluProAsnAsnLysLysAsnLysGluAsnProCysValGluIleTyrrIle 134
  |||
466 TGAGGCCCAACAACAAGAACAGACAGAGACGCGGAGATCTATATCA 515
134 ySarGAsnLysAspAlaGlyLysTrrPAsnAspAspAlaCysHsLysLeu 150
  |||
516 AGAGAAACAAGATGACAGCAATGGAACGATGACGCCCTGCCAACAACAT 565
151 LysAlaAlaLeuCySrrTyrrThraLaserCysGlnProTrrPserCysSerc 167
  |||
566 AAGCAGAGCCCTCTGTACACAGCTTCTGCCAGCCCTGCTCATTCAGTGG 615
167 yHisGlyGluCysValGluIleIleAsnAsnHsThrCysAsnCysAspY 184
  |||
616 CCATGAGAAATGCTAGAAATCATCAATTAATTAACACTGCAACTGTGATG 665
184 aIleTyrrTyrcylProGlnCysGlnLeuValIleGlnCysGluProLeu 200
  |||
666 TGGGTACTATGGGCCCCAGTGTCACTTGTGATTCAGTGTGAGCCCTTGG 715
201 GluAlaProGluLeuGlyThrMetAspCysTrrHsProPheGlyAsnPh 217
  |||
716 GAGGCCCCAGAGCTGGGTACCATGACATGTACTCACCCCTTGGGAAACT 765
217 eSerPheSerSerGlnCysAlaPheSerCysSercGluTyrrAsnLeuT 234
  |||
766 CAGCTTCAGCTCACAGTGTCCCTTCAGCTGCTTGAAGAAACAACCTTAA 815
234 hrGlyIleGlnGluThrThrCysGlyProPheGlyAsnTrrPserSerPro 250
  |||
816 CTGGGATTGAGAAACACACCTGTGGACATTTTGGAAACTGGTCACTCCA 865
251 GluProThrCysGlnValIleGlnCysGluProLeuSerAlaProAspLe 267
  |||
866 GAACCAACCTGTCAAGTATTCAAGTGTAGCCCTTATCAGCACCAAGATT 915
267 uGlyIleMetLanCysSerHsAspLeuAlaSerPheSerPheThrSerA 284
  |||
916 GGGCATCATGAACCTGTAGCAATCCCTGCCAGCTTTCAGCTTACCTCTG 965

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284 lAcysThrPheIleCysSerGluGlyThrGluLeuIleGlyLysLys 300
  |||
966 CATGTACTTCATCTGCTCAGAAAGAACTGAGTTATTTGGAAAGAA 1015
301 ThrIleCysGluSerSerGlyIleTrrPserAsnProSerProIleCysG 317
  |||
1016 ACCATTGTGAAATCATCTGGAATCTGTGCAAAATCCYAGTCCAAATATGTCA 1065
317 nLysLeuAspLysSerPheSerMetIleLysGluGlyAspTyrrAsnProL 334
  |||
1066 AAAATTGGACAAAAGTTTCTCAATGATTAAGAGGGGTGATTTTAAACCC 1115
334 euPheIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
  |||
1116 TCTTCATTCCAGTGGCAGATCATGTTACTGCAATTCCTGGTTGGCATTT 1165
351 IleIleTrrPLeuAlaArgArLeuLysLysGlyLysLysSerLysArgSe 367
  |||
1166 ATCATTTGGCTGGCAAGAGAGATTAATAAAGCAAGAAATCCACAAGAGAG 1215
367 rMetAsnAspProTyrr 372
  |||
1216 TATGAATGACCCCATAT 1231

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seq_name: /cgn2_6/ptodata/2/pna/US6021_COMB.seq:US-60-213-360-1118

seq_documentation_block:

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: Sequence 1118, Application US/60213360
: GENERAL INFORMATION:
: APPLICANT: Morris, Macdonald
: APPLICANT: Lal, Preeti
: APPLICANT: Diep, Dinh
: TITLE OF INVENTION: Method for the identification of Sequence Polymorphisms Using
: TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Poly
: FILE REFERENCE: GX-0014 P
: CURRENT APPLICATION NUMBER: US/60/213,360
: CURRENT FILING DATE: 2000-06-21
: NUMBER OF SEQ ID NOS: 8347
: SOFTWARE: PERL Program
: SEQ ID NO 1118
: LENGTH: 2385
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: 331616.2
US-60-213-360-1118

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alignment_scores:

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Quality: 2090.00 Length: 372
Ratio: 5.633 Gaps: 0
Percent Similarity: 99.731 Percent Identity: 98.925

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alignment_block:

US-09-119-209-2 x US-60-213-360-1118 ..

Align seg 1/1 to: US-60-213-360-1118 from: 1 to: 2385

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1 MetIlePheProTrrPlyScySglInSerThrGlnAtrGAspLeuTrrPAsnI 17
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137 ATGATAATTTCCATGTGAAATGTGAGAGCACCCAGAGGACTTATGTGAACAT 186
17 ePheLysLeuTrrPglYTrPThrMetLeuCyScyAspPheLeuAlaHisH 34
  |||
187 CTTCACAGTTGTGGGGGTGGACAAATGCTCTGTGTGTATTTCTGGCACATC 236
34 IsGlyThrTyrcysTrrPThrThrsTySercGluLysProMetAsnTrrP 50
  |||
237 ATGGAACGACGACTGCTGACTTACCATTTATTCGAATAAACCCATGAACTGG 286
51 GlnAtrGAlaAtrGArpPheCysAtrGAspAsnTyrrThrAspLeuValAla 67

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|||||
287 CAAAGGGCTAGAGATCTGCCGAGACATATACAGATTAGTGGCAT 336
67 egluasnlysaliagluilegyluTyrluGluLysThleuProphesera 84
|||||
337 ACMAAACAGGCGGAATGAGTATCTGGAGAAAGACCTGCTTCAGTC 386
84 rgseryTyrrpIleglyllearglysIleglyglyIletrpThrTrp 100
387 GTTCTTACTACTGATAGGATCCGGAAGATGAGAGAAATATGACCTGG 436
101 ValglyThrasnLysSerleuThglGluIuAgluasnTrpGlyaspG1 117
437 GTGGGAACCAACAAATCTTACTGAGAAAGCAGAGAACTGGGAGATGG 486
117 ygluProasnLysLysLysasnLysGluaspGysValGluIleTyrlleL 134
487 TGAGCCCAACACAAAGAAAGAAAGAGAGAGCTGGTGAATCTATATCA 536
134 ysarGasnLysaspAlaglyLysTrpasnAspAlaCysHsLysLeu 150
537 AGAGAAACAAAGATGCAGGCAATGGAACATGACCGCTGCCAAACTA 586
151 LysAlaAlaLeucystyrrThraLaserCysGlnProtrpserCysserG1 167
587 AAGGCAACCTCTGTITACACAGCTTCTGCGACGCTGCTCATGCACTGG 636
167 yHsIsglyGluCysValGluIleleasnAsnHsTrpCysAsnGysAspV 184
637 CCATGGAGATGTGTGAAATCATCAATATATACACCTGCMACTGTGATG 686
184 aIglyTyrrpGlyProGlnCysGlnLeuValIleGlnCysGluProLeu 200
687 TGGGGTACTATGGGCCCGCCAGTGTGACTTGTGATTCAGTGTGAGCCTTGG 736
201 GluAlaProGluLeuGlyThrmelaPcysThraHsProPhGlyAsnph 217
737 GAGGCCCAAGAGTGGTACCATGACCTACTCACCCCTTTGGAAACTT 786
217 eSerPheSerSerGlnCysAlaPheSerCysSerGluGlyThraSnLeuT 234
787 CAGCTTCACATCAGATGCTGCTCAGTGTGCTGAGAGAACAACTTAA 836
234 hcglylleGluGluThrThrCysGlyProPhGlyAsnTrpserSerPro 250
837 CTGGGATTAAAGAAACACCTGTGTGACATTTGGAACCTGTCACTCCA 886
251 GluProThrCysGlnValIleGlnCysGluProLeuSerAlaProaspLe 267
887 GAACCAACCTGTCAAGTATTCAGTGTGAGCCTCATCAGCACCGATTT 936
267 uGlylleMetasnCysSerHisProLeuAlaSerPheSerPheThrSera 284
937 GGGGATCATGAACCTGTACCATCCCTGCGCAGCTTCAGCTTACCTCTG 986
284 IacysThrPheIleCysSerGluGlyThrGluLeuIleGlyLysLys 300
987 CATGTACTCTATCTGCTCACAAGACACTGAGTTAATTGGGAAAGAA 1036
301 ThrIleCysGluSerSerGlyIleTrpSerAnProSerProIleCysG1 317
1037 ACCATTGTGATCATCTGGAATCTGGTCAATCTCTAGTCCAAATATGTCA 1086
317 nLysLeuaspLysSerPheSerMetIleLysGluGlyAspTyrrAsnProL 334
1087 AAAATTTGGACAAAGTTTCTCAATGATTAGGAGGTTATTAACCCCC 1136
334 eupheileProValAlaValMetValThraLapheSerGlyleuAlaPhe 350
1137 TCTTCATTTCCAGTGCAGACTATGTTACTGCTATTTCTGGGTTGGCA 1186
351 IleleIrrpleuAlaArgLeuLysGlyLysLysSerLysArgse 367
|||||

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1187 ATCATTTGCTGGCAAGAGATTAATAAAGCAGAAATCCAGAGAG 1236
367 rMetasnAspProTyrr 372
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1237 TATGATATGACCATAT 1252
seq_name: /cgn2_6/prodata/2/pna/us6024_COMB.seq:us-60-243-521-8
seq_documentation_block:
; Sequence 8, Application US/60243521
; GENERAL INFORMATION:
; APPLICANT: Hopkins, Christopher M.
; APPLICANT: Peterson, David P.
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES REGULATED IN ACTIVATED T CELLS
; FILE REFERENCE: PA-0042 P
; CURRENT APPLICATION NUMBER: US/60/243,521
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PERL Program
; SEQ ID NO 8
; LENGTH: 2385
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Template ID: 331616.2
US-60-243-521-8

alignment_scores:
Quality: 2090.00 Length: 372
Ratio: 5.633 Gaps: 0
Percent Similarity: 99.731 Percent Identity: 98.925

alignment_block:
US-09-119-209-2 x US-60-243-521-8

Align seg 1/1 to: US-60-243-521-8 from: 1 to: 2385

1 MetIlePheProTrpLysCysGlnSerThrGlnArgAspLeuTrpasn1 17
|||||
137 ATGATATTTCATGGAATGTGACAGCACCGAGGAGATTGTGAACT 186
17 ePheLysLeuTrpGlyTrpThrmelaCysCysAspPheleuAlaHsH 34
|||||
187 CTTCAGATTGTGGGGGTGAGACATGCTGTGTGTGATTTCTGCGCACATC 236
34 IsglyThrTyrrCysTrpThrTyrrHisTyrrSerGluLysProMetAsnTrp 50
|||||
237 ATGGAACCGACTGCTGACTTACCATTTATTTGAAAAACCATGAGACTGG 286
51 GluArgAlaArgArgPheCysArgAspAsnTyrrThraspLeuValAla1 67
|||||
287 CAAAGGGCTAGAAGATTCTGCCGAGACAAATATACACAGATTAGTGGCAT 336
67 egluasnlysaliagluilegyluTyrluGluLysThleuProphesera 84
|||||
337 ACMAAACAGGCGGAATGAGTATCTGGAGAAAGACCTGCTTCAGTC 386
84 rgseryTyrrpIleglyllearglysIleglyglyIletrpThrTrp 100
387 GTTCTTACTACTGATAGGATCCGGAAGATGAGAGAAATATGACCTGG 436
101 ValglyThrasnLysSerleuThglGluIuAgluasnTrpGlyaspG1 117
|||||
437 GTGGGAACCAACAAATCTTACTGAGAAAGCAGAGAACTGGGAGATGG 486
117 ygluProasnLysLysLysasnLysGluaspGysValGluIleTyrlleL 134
|||||
487 TGAGCCCAACACAAAGAAAGAAAGAGAGAGACTGGTGAATCTATATCA 536

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134 ysArGAsnLysAspAlaGlyLysTrpAsnAspAlaCysHisLysLeu 150
|||||
537 AGAGAAACAAAGATGCGCAAAATGGAAAGATGACGCTGCCCAAACTA 586
151 LysAlaAlaLeuCysTrpThrAlaSerCysGlnProTrpSerCysSerL 167
|||||
587 AAGGACAGCCCTCTGTTACACAGCTTCTTCCAGCCCTGGTGTACAGCTGG 636
167 yHisGlyGlyCysValGluIleLeuAsnAsnHisThrCysAsnCysAspY 184
|||||
637 CCATGAGAAATGTGTGAATATCATCAATATTAACACCTGCACACTGGATG 686
184 aIGlyTyrTrpGlyProGlnCysGlnLeuValIleGlnCysGlnProLeu 200
|||||
687 TGGGGTACTATGGGCCCCAGTGTCACTGTGTGATTCAGTGTGAGCCTTGG 736
201 GluAlaProGlnLeuGlyThrMetAspCysThrHisProPhelLysnph 217
|||||
737 GAGCCCCCAGAGCTGGGTACCATGACCTGTACTACCCCTTTGGGAAACTTT 786
217 eSerPheSerSerGlnCysAlaPheSerCysSerGlnGlyThrAsnLeuT 234
|||||
787 CAGCTTCACACTCACAGTGTGCTTCAGCTGCTGTGAAGAGAACAACTTA 836
234 hGlyIleGlnGluThrThrCysGlyProPhelGlyAsnTrpSerSerPro 250
|||||
837 CTGGGATGTGAAGAAACCACTGTGACCATTTGGAAACTGTGTCATCTCCA 886
251 GluProThrCysGlnValIleGlnCysGlnProLeuSerAlaProAspLe 267
|||||
887 GAACCAACCTGTCAAGTCAATGAGTTCAGCTTCAGCTTATCAGCACAGACTTT 936
267 uGlyIleMetAsnCysSerHisProLeuAlaSerPheSerPheThrSera 284
|||||
937 GGGGATCATGAACCTGTAGCCATCCCTGGCCAGCTTCACCTTACTCTTG 986
284 IaCysThrPheIleCysSerGlnGlyThrGluLeuIleGlyLysLysLys 300
|||||
987 CATGTACCTTCATCTGCTCAGAAAGAACTGATTAATGGGAAAGAA 1036
301 ThrIleCysGlnSerSerGlyIleTrpSerAsnProSerProIleCysGln 317
|||||
1037 ACCATTGTGGAATCAATCGGAATCTGGTCAAAATCCAGTCCAAATAGTCA 1086
317 nLysLeuAsnLysSerPheSerMetIleLysGlnGlyAspTyrAsnProL 334
|||||
1087 AAAATTGGCAAAAGTTTCTCATGATTTAAGAGGGGTGATTATACCCCC 1136
334 euPheIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
|||||
1137 TCTTCACTTCAGTGGCAGTCATGTTACTGCAATTCCTGGTTGGCATTT 1186
351 IleIleTrpLeuAlaArgArgLeuLysLysGlyLysLysSerLysArgSe 367
|||||
1187 ATCAATTGGCTCGCAAGAGATTAAAAAAGCAGAAATCCAAGAGAAG 1236
367 rMetAsnAspProTyr 372
|||||
1237 TATGAATGACCAATAT 1252

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seq_name: /cgn2_6/ptodata/2/pna/US093_COMB.seq:US-09-396-970-8480

seq_documentation_block:

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: Sequence 8480, Application US/09396970
: GENERAL INFORMATION:
: APPLICANT: Geating, David P.
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
: FILE REFERENCE: MLN98-409A
: CURRENT FILING DATE: 1999-09-14
: EARLIER APPLICATION NUMBER: 60/100,293

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: EARLIER FILING DATE: 1999-09-14
: NUMBER OF SEQ ID NOS: 8756
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 8480
: LENGTH: 2564
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: (1)---(2564)
: OTHER INFORMATION: n - A,T,C or G
US-09-396-970-8480

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alignment_scores:
    Quality: 2090.00      Length: 372
    Ratio: 5.633          Gaps: 0
    Percent Similarity: 99.731    Percent Identity: 98.925

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alignment_block:

US-09-119-209-2 x US-09-396-970-8480 ..

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Align seg 1/1 to: US-09-396-970-8480 from: 1 to: 2564

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155 ATGATATTTTCATGGAATAGTCAGAGCACCAGAGGAGCTTATGGAACAT 204
17 ePheLysLeuTrpGlyTrpThrMetLeuCysCysAspPheLeuAlaHis 34
|||||
205 CTTCAGAGTTGTGGGGGTGACAAATGCTCTGTGTGTATTCCTGGCACATC 254
34 IaGlyThrTrpCysTrpThrTrpHisIstYrSerGlnLysProMetAsnTrp 50
|||||
255 ATGGAACCGACTGTGGACTTACCATTAATTCGAAAAACCATGAACCTGG 304
51 GlnArgAlaArgArgPheCysArgAspAsnTyrThrAspLeuValAla11 67
|||||
305 CAAGGCGTAGAAGATTCGCGGAGCATTTACAGATTTAGTTCCTCAT 354
67 eGlnAsnLysAlaGluIleGlyThrLeuGluLysThrLeuProPheSera 84
|||||
355 ACAAAACAAGCGCGGAATTCAGATCTCGAGAAAGACTCTGCCCTTCACATC 404
84 rSerSerTrpTrpIleGlyIleArgLysIleGlyGlyIleThrProPheTrp 100
|||||
405 GTTCTTACTACTGATGAGAAATCCGGAAATAGAGAAATATGAGACGTGG 454
101 ValGlyThrAsnLysSerLeuThrGlnGluAlaGluAsnTrpGlyAspG1 117
|||||
455 GTGGGACCAACAATCTCTTACTGAAGAACAGAACTGGGGAGATGG 504
117 yGluProAsnAsnLysLysAsnLysGlnAspCysValGluIleTyrIleL 134
|||||
505 TCAGGCCCAACAACAAGAAACAAGACGAGCATCGCGAGATCTATATCA 554
134 ysArgAsnLysAspAlaGlyLysTrpAsnAspAlaLacHisLysLeu 150
|||||
555 AGAGAAACAAGAATGAGGCAATGGAAAGATGACCGCTGCCCAAACTA 604
151 LysAlaAlaLeuCysTrpThrAlaSerCysGlnProTrpSerCysSerL 167
|||||
605 AAGGACAGCCCTCTGTTACACAGCTTCTTCCAGCCCTGGTCAATGCACTGG 654
167 yHisGlyGlyCysValGluIleLeuAsnAsnHisThrCysAsnCysAspY 184
|||||
655 CCATGAGGAATGTGTGAATATCATCAATATTAACACCTGCACACTGGATG 704
184 aIGlyTyrTrpGlyProGlnCysGlnLeuValIleGlnCysGlnProLeu 200
|||||
705 TGGGGTACTATGGGCCCCAGTGTCACTGTGTGATTCAGTGTGAGCCTTGG 754
201 GluAlaProGlnLeuGlyThrMetAspCysThrHisProPhelGlyAsnph 217

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|||||
755 GAGGCCCGAGAGCTGGTACCATGACGTACTACCCCTTGGGAAACTT 804
217 eSerPheSerGlnCysAlaPheSerCysSerGluGlyThrSerLeuT 234
805 CAGCTTCAGCTCAGAGTGTGCTTACGCTCTGTAAGGAACAACATTAA 854
234 hrGlyTlEgIuGluThrThrCysGlyPropheGlyAsnTrpSerSerPro 250
855 CTGGGATTGGAAGAAACCACTGTGTGACCATTTGGAAACTGTCATCTCCA 904
251 GluProThrCysGlnValIleGlnCysGluProLeuSerAlaProAspLe 267
905 GAAACCACTCTCAAGTATTCAGTGTGAGCCCTCTATCAGACACAGATT 954
267 uGlyTlEMeTasnCysSerHisProLeuAlaSerPheSerPheThrSera 284
955 GGGGATCATGAAGCTGTAGCCATCCCTGGCCAGCTTACGTTTACCTCTG 1004
284 lAcylThrPheIleCysSerGluGlyThrGluLeuIleGlyLysLys 300
1005 CATGTACCTTCACTGTCTCAGAAAGAACTGAGTTAATTGGGAAGAA 1054
301 ThrIleCysGluSerSerGlyIleTrpSerAsnProSerProIleCysG 317
1055 ACCATTGTGATCATCTGGAATCTGTCAAAATCCTAGTCCAAATATGTCA 1104
317 nLysLeuAspLysSerPheSerMetIleLysGluGlyAspTyrAsnProI 334
1105 AAATTGTGCAAAAGTTTCTCAATGATTAAGAGGATGATTATACCCCC 1154
334 eUpheIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
1155 TCTTCATTCAGTGGCAGTCATGATGTACTGCAATTCCTGGTGGCATTT 1204
351 lIleIleTrpLeuAlaArgArgLeuLysLysGlyLysSerLysArgSe 367
1205 ATCATTTGGCTGGCAAGAGATTAAAAAAGCAAGAAATCCAAAGGAAG 1254
367 rMeTasnAspProTyr 372
1255 TATGAATGACCCCATAT 1270

seq_name: /cgn2_6/plodata/2/pna/US6017_COMB.seq:us-60-172-373-15742

seq_documentation_block:
; Sequence 15742, Application US/60172373
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: Method for the identification of Sequence Polymorphisms Using
; FILE REFERENCE: GX-0006_P
; CURRENT APPLICATION NUMBER: US/60/172,373
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 15742
; LENGTH: 2387
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 331616.2
US-60-172-373-15742

alignment_scores:
Quality: 2082.00 Length: 372
Ratio: 5.627 Gaps: 0
Percent Similarity: 99.462 Percent Identity: 98.656

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alignment_block:
US-09-119-209-2 x US-60-172-373-15742
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139 ATGATATTTTCCATGGAAATGTGAGAGCAACCCAGAGGAGCATATGAAACAT 188
17 ePheLysLeuTrpGlyTrpThrMetLeuCysCysAspPheLeuAlaHis 34
189 CTTCAGTTGTGGGGGTGGACATCTCTGTTGTGATTTCTGCGCACATC 238
34 lEgIYThrTyrCysTrpThrTyrHisTyrSerGluLysProMetAsnTrp 50
239 ATGGAACCGACGCTGTGACTTACCATTTATCTGAAAAAACCATGAACTGG 288
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167 yHisGlyGluCysValGluIleIleAsnAsnHisThrCysAsnCysAspV 184
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Sequence 292, Application US/60118318
GENERAL INFORMATION:
APPLICANT: Roopa, Reddy
APPLICANT: Guejler, Karl, J.
APPLICANT: Au-Young, Janice
TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED H
FILE REFERENCE: PA-0013 P
CURRENT APPLICATION NUMBER: US/60/118, 318
CURRENT FILING DATE: 1999-02-01
NUMBER OF SEQ ID NOS: 306
SOFTWARE: PERL Program
SEQ ID NO 292
LENGTH: 2385
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: 1876370CB1
US-60-118-318-292

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Ratio: 5.604 Gaps: 0
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: Sequence 1, Application PC/TUS9203970
: GENERAL INFORMATION:
: APPLICANT: Dana-Farber Cancer Institute, Inc.
: TITLE OF INVENTION: LEUKOCYTE-ASSOCIATED CELL SURFACE
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSER: Weingarten, Schurgin, Gagnebin & Hayes
: STREET: Ten Post Office Square
: CITY: Boston
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US92/03970
: FILING DATE: 19920513
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Heine, Holliday C.
: REGISTRATION NUMBER: 34,346
: REFERENCE/DOCKET NUMBER: DFCI-152Bq9
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 542-2290
: TELEFAX: (617) 451-0513
: TELEX: 940675
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2330 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 53..1210
: PUBLICATION INFORMATION:
: DOCUMENT NUMBER: US 07/700,773
: FILING DATE: 15-MAY-1991
PCT-US92-03970-1

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Ratio: 5.611 Gaps: 0
Percent Similarity: 99.462 Percent Identity: 98.118

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; Sequence 1, Application US/08008459
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; TITLE OR INVENTION: KANSAS, Geoffrey S.
; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMUL'TANEOUS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurigin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/008,459
; FILING DATE: 25-JAN-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,606
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/862,483
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,608
; FILING DATE: 03-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/737,092
; FILING DATE: 29-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/730,503
; FILING DATE: 08-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/700,773
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/313,109
; FILING DATE: 21-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Heine, Holliday C.
; REGISTRATION NUMBER: 34,346
; REFERENCE/DOCKET NUMBER: DFCI-318XX
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: (617) 542-2290
; TELEFAX: (617) 451-0313
; TELEX: 940675
; INFORMATION FOR SFO ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2330 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
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; LOCATION: 53..1210
; US-08-008-459-1

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Ratio: 5.611 Gaps: 0
Percent Similarity: 99.462 Percent Identity: 98.118

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seq_documentation_block:
; Sequence 1, Application US/08340539
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; APPLICANT: Kansas, Geoffrey S.
; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
; TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,539
; FILING DATE: 16-NOV-1994
; CLASSIFICATION: 514

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,459
; FILING DATE: 25-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,606
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/862,483
; FILING DATE: 02-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,608
; FILING DATE: 03-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/737,092
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; FILING DATE: 08-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/700,773
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/313,109
; FILING DATE: 21-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Heine, Holliday C.
; REGISTRATION NUMBER: 34,346
; REFERENCE/DOCKET NUMBER: DECI-318XX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-2290
; TELEFAX: (617) 451-0313
; TELE: 940675
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2330 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 53..1210
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US 07/700,773
; FILING DATE: 15-MAY-1991
; US-08-340-539-1

alignment_scores:
Quality: 2076.00 Length: 372
Ratio: 5.611 Gaps: 0
Percent Similarity: 99.462 Percent Identity: 98.118

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US-09-119-209-2 x US-08-340-539-1 ..

Align seg 1/1 to: US-08-340-539-1 from: 1 to: 2330
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92 ATGATATTTCCTCATGGAATGTGACAGACCCGAGAGGACTTATGGAACT 141
17 ePheLysLeuTrpGlyTrpThrMetLeuCysCysAspPheLeuAlaHis 34
|||||.....
142 CTTCAGATTGTGGGGGTGGACAATGCTGTGTGATTTCCTGGCACATC 191
34 IsGlyThrTyrCysTrpThrTyrHisTyrSerGluLysProMetAsnTrp 50
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192 ATGAAACCGACTGTGGACTTATTCATTTGAAAAACCCATGAACTGG 241
51 GlnArgAlaArgArgPheCysArgAspAsnTyrThrAspLeuValAla 67

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242 CAAAGGCTAGAGATTCGCCGAGACATACACAGATTAGTTGCCAT 291
67 eglAsnLysAlaGluIleGluuTyrlLeuGluLysThrLeuProPheSera 84
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292 ACAAAACAAGCCGGAATTCGATCTGGAGAAAGACTCTGCCCTTTCATGC 341
84 rGSeTyrrTyrrPLeGlylleArGlylleGlylleTyrrPLeu 100
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342 GTTCTTACTACTGGATAGGAATCCGGAAGATAGAGAAATATGACCTGCG 391
101 ValGlyThrAsnLysSerLeuThrGluAlaGluAsnTrpGlyaspG1 117
|||||
392 GTGGGAACCAACAATCTCTCACTGGAAGAGACAGAACTGGCGAGATGCG 441
117 yGluProAsnAsnLysAsnLysGluAspGlyValGluIleTyrrLeu 134
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442 TGAAGCCCAACAACAAGACAAGACGACTCGTGAGATCTATATATCA 491
134 ySarGAsnLysAspAlaGlyLysTrpAsnAspAspAlaCysHisLysLeu 150
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492 AGAGAAACAAGATGACGCAATGGAAGATGACGCTGCCACAACATA 541
151 LysAlaAlaLeuGlyThrAlaSerGlyInProTrpSerGlySerg1 167
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542 AAGCGAGCCCTCTGTACACAGCTTCTGCCAGCCCTGGTCATGCACTGG 591
167 yHisGlyGlyCysValGluIleLeuAsnAsnHisThrCysAsnCysAspV 184
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592 CCATGGAGAGATGTGTGAATATCATCAATATTAACACCTCCAACTGATG 641
184 aGlyTyrrTyrrGlyProGlnCysGlnLeuValIleGlnCysGlnProLeu 200
|||||
642 TGGGGTACTATGGGCCCGCAGTGTGATGATTCAGTGTGAGCCTTGG 691
201 GluAlaProGluLeuGlyThrMetAspCysThrHisProPheGlyAsnPh 217
|||||
692 GAGGCCCGCAGACTGGTACCATGGACGTACTACACCTTGGGAAACTT 741
217 eSerPheSerSergInCysAlaPheSerCysSergInGlyThrAsnLeuT 234
|||||
742 CAAGTTCACATCAGAGTGTGCTTCCAGCGCTCAGAGAAACAACCTTAA 791
234 hrcGlyIleGlnIuThrThrCysGlyProPheGlyAsnTrpSerSergPro 250
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792 CTGGAGTTGAAGAAACCACTGTGAACTTTGAACTGTGATCATCTCCA 841
251 GluProThrCysGlnValIleGlnCysGlnProLeuSerAlaProAspLe 267
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267 uGlyIleMetLanCysSerHisProLeuAlaSerPheSerPheThrSera 284
|||||
892 GGGGATCATGAACGTGTACCATCCCTGGCAGCTTCAGCTTTACCTGTG 941
284 laCysThrPheIleCysSergInGlyThrGluLeuIleGlyLysLysLys 300
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942 CATGTACTTCACTGTCTCAAGAAAGACTGAGTTAATTGGGAAAGAA 991
301 ThrIleCysGluSerSergIleTrpSerAsnProSerProIleCysG1 317
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992 ACCATTTGTGAATCATCTGGAATCTGGTCAAAATCTCTATCCAAATATGCA 1041
317 nLysLeuAspLysSerPheSerMetIleLysGlyGlyAspTyrrAsnProL 334
|||||
1042 AAAATTTGGACAAAAGTTTCTCAATGATTAAAGAGGATGATTATAACCCC 1091
334 cupheIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
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1092 TCTTCATTTCCAGTGGACGTCACTGATCTGATCTCTGGGTTGGCAATT 1141
351 lleIleTrpLeuAlaArgArgLeuLysGlyLysLysSerLysArgSe 367
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1192 TATGAATGACCATAT 1207

seq_name: /cgn2_6/ptodata/2/pma/US084_COMB.seq:US-08-410-569-1
seq_documentation_block:
; Sequence 1, Application US/08410569
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; APPLICANT: Spertini, Olivier G.
; TITLE OF INVENTION: LEUCOCYTE ADHESION MOLECULE-1 (LAM-1)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,569
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,608
; FILING DATE: 03-OCT-1991
; APPLICATION NUMBER: US 07/700,773
; FILING DATE: 15-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heine, Holliday C.
; REGISTRATION NUMBER: 34,346
; REFERENCE/DOCKET NUMBER: DFCG-152EX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-2290
; TELEFAX: (617) 451-0313
; TELEX: 940675
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2330 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 53..1210
; US-08-410-569-1

alignment_scores:
quality: 2076.00 length: 372
Ratio: 5.611 Gaps: 0
Percent Similarity: 99.462 Percent Identity: 98.118

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Align seg 1/1 to: US-08-410-569-1 from: 1 to: 2330

1 MetIlePheProTrpLysCysGlnSerThrGlnArgAspLeuTrpAsnI1 17
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92 ATGATATTTTCATGGAATGTCAGAGACACCCAGAGGAGACTTATGGAACAT 141

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34 lsglyThrTyrCysTrpPheTrpHisTyrSerGluLysProMetLsnTrp 50
192 ATGGAAACCGACTGCTGGACTTACATTAATTCGAAAACCCATGAACTGG 241
51 GlnATGAlaArgArgPheCysArgAspAsnTyrThrAspLeuValAlaI 67
242 CAAAGGGCTAGAGATTTCTCCGAGACAAATTACACGATTAGTGGCCAT 291
67 eglAsnLysAlaGluIleGluTyrLeuGluLysThrLeuProPheSerA 84
292 ACAAAACAAGCGGGAATTTGAGTATCTGGAGAAAGACTGCTTCACATC 341
84 rgseryTyrTrpIleGlyIleArgLysIleGlyIleTrpThrTrp 100
342 GTTCTTACTACTGGATAGGAATCCGGAAGATAGGAGAAATATGACGTG 391
101 ValGlyThrAsnLysSerleuThrGluGluAlaGluAsnTrpGlyAspG 117
392 GTGGGAACCAACAATCTCTCACTGAAGAGCAAGAACTGGGGAGATGG 441
117 ygluProAsnAsnLysLysAsnLysGluAspCysValGluIleTyrIleL 134
442 TCAGCCCAACAACAAGAAACAAGAGAGACTGCGTGGAGATCTATATCA 491
134 ysArgAsnLysAspAlaGlyLysTrpAsnAspAlaCysHisLysLeu 150
492 AGAGAAACAAGATGACAGCAATGGAACGATGACGCTGCACAAACTA 541
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542 AAGGAGCCCTCTGTACACAGCTTCTGCGACGCTTGCTCATGACATGG 591
167 yHisGlyGluCysValGluIleIleAsnAsnHisThrCysAsnCysAsp 184
592 CCATGGAGAAATGCTGAAGAATCATCATTAATTACACCTGCACATGTGAT 641
184 aGlyTyrTyrGlyProGlnCysGlnLeuValIleGlnCysGluProLeu 200
642 TGGGTACTATGCGCCCACTGCTCAGTTGTGATTCAGTGTGAGCCTTGG 691
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942 CATGATACCTTCATCTGCTCAGAAAGAACTGAGTTAATTGGGAAGAA 991
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334 euPheIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
1092 TCTTCACTTCAGTGGCAGTCATGTTACTGTCATTTCTGGGTTGGCATTT 1141
351 IleIleTrpLeuAlaArgArgLeuLysLysGlyLysSerLysArgS 367
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367 rMetAsnAspProTyr 372
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seq_name: /cgn2_6/p/ctdata/2/pna/US6021_COMB.seq:US-60-212-659-816

seq_documentation_block:
: Sequence 816, Application us/60212659
: GENERAL INFORMATION:
: APPLICANT: Beasley, Ellen
: TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
: FILE REFERENCE: CLO00674
: CURRENT APPLICATION NUMBER: US/60/212,659
: NUMBER OF SEQ ID NOS: 879
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 816
: LENGTH: 3238
: TYPE: DNA
: ORGANISM: HUMAN
US-60-212-659-816

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Quality: 1883.00 Length: 345
Ratio: 5.538 Gaps: 0
Percent Similarity: 98.551 Percent Identity: 97.391

alignment_block:
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Align seg 1/1 to: US-60-212-659-816 from: 1 to: 3238

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38 sTrpThrTyrHisTyrSerGluLysProMetAsnTrpGlnArgAlaArgA 55
1861 CTGGACTTACCATTAATTCTGA AAAACCCATGAATGCGCAAAAGGGCTAGA 1910
55 rgPheCysArgAspAsnTyrThrAspLeuValAlaIleLsnLysAla 71
1911 GATTCGCCGAGACAATTACACAGATTGATTCATACAAAACAAGGGC 1960
72 GluIleGluTyrLeuGluLysThrLeuProPheSerArgSerTyrTyrTr 88
1961 GAAATTGAGTATCTGAGAGAACTGCTGCTTCACTGCTTACTACTAG 2010
2011 GATAGGAATCCCGAAGATAGGAGAAATATGACGTGGGGGAGAACCA 2060
105 ySerLeuThrGluGluAlaGluAsnTrpGlyAspGlyGluProAsn 121
2061 AATCTCTTACTGAGAGACGAGAACTGCGGAGATGTACCCCAACAC 2110
122 LysLysAsnLysGluAspCysValGluIleTyrIleLysArgAsnLysAs 138

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2111 AAGAGAACAGAGAGACTGCTGGAGATCTATATCAAGAGAACCAAGA 2160
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2161 TCCAGGCAAAATGGAACGATGAGCCCTGGCACAACTAAAGCAGCCCTCT 2210
155 ySTy-ThrAlaSerCysGlnProTTPSerCysSerGlyHisGlyGluCys 171
2211 GTTACACAGACTCTTGGCCAGCCCTGGTCATCAGTGGCCATGAGAAATGT 2260
172 ValGluLeuLeuAsnAsnHisThrCysasnCysAspValGlyTyrTyrGlu 188
2261 GTAGAAATCATCAATTAATTAACCTGCACACTGTATGTGGGGTACTATGG 2310
188 yProGlnCysGlnLeuValIleGlnCysGluProLeuGluAlaProGluL 205
2311 GCCCAGAGTGCAGCTTGTGATTCAGTGTGAGCCCTTGGAGGCCCCAGAGC 2360
205 euGlyThrMetAspCysThrHisProPheGlyAsnPheSerPheSerSer 221
2361 TGGGTACCATGACTGTACTACCTTTGGGAAACTTCACCTTCACGCTCA 2410
222 GlnCysAlaPheSerCysSerGluGlyThrAsnLeuThrGlyIleGluGlu 238
2411 CAGTGTGCTTCAGCTGCTCTGAAGAGAACTTAACCTGGATGAGAGA 2460
238 uThrThrCysGlyProPheGlyAsnTTPSerSerProGluProThrCysG 255
2461 AACCACTGTGGACCATTTGGAACCTGTGCATCTCCAGAACCAACCTGTC 2510
255 InValIleGlnCysGluProLeuSerAlaProAspLeuGlyIleMetLan 271
2511 AAGGATTCAGTGTGAGCCCTCATCAACCACTTTGGGGATCATGAAAC 2560
272 CysSerHisProLeuAlaSerPheSerPheThrSerAlaCysThrPheI 288
2561 TGTAGCCATCCCTGGCCAGCTTCACCTTACCTGATGATCACTTCAT 2610
288 eCysSerGluGlyThrGluLeuThrIleGlyLysLysLysThrIleCysGlu 305
2611 CTGCTCAGAAAGAACTGAGTTAATTTGGGAAGAAACCACTTTGTGAAT 2660
305 eISerGlyIleTTPSerAsnProSerProIleCysGlnLysLeuAspLys 321
2661 CATCTGGAATCTGGTCAATCTCAAGTCAATATGTCACAAATTTGACAAA 2710
322 SerPheSerMetIleGlyGlnGlyAspTyrAsnProLeuPheIleProVa 338
2711 AGTTTCTCAATGATTAGAGAGGATTAATACCCCTTCATTCACAGT 2760
338 AlaValMetValThrAlaPheSerGlyLeuAlaPheIleIleTPrLeuA 355
2761 GCACAGTCATGTTACTGCATTCCTCGGGGTGGCATTTATCATTTGGCTGG 2810
355 IaIrGArGleuLysLysGlyLysLysSerLysArg 366
2811 CAAGAGAGATTAAAAAAGCAAGAAATCCACAGACA 2845
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seq_documentation_block:
: Sequence 3, Application US/09119209
: GENERAL INFORMATION:
: APPLICANT: LASKY, LAURENCE A.
: APPLICANT: STACHELL, SCOTT E.
: APPLICANT: ROSEN, STEVEN D.
: APPLICANT: SINGER, MARK S.
: APPLICANT: YEDNICK, TED A.
: TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way

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: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WinPatIn (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/119,209
: FILING DATE: 20-Jul-1998
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/513278
: FILING DATE: 10-Aug-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/059027
: FILING DATE: 6-MAY-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/786149
: FILING DATE: 31-OCT-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/315015
: FILING DATE: 23-FEB-1989
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
: REGISTRATION NUMBER: 34,659
: REFERENCE/DOCKET NUMBER: P0565D1C3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-5530
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2214 base pairs
: TYPE: Nucleic Acid
: STRANDEDNESS: Single
: TOPOLOGY: Linear
: us-09-119-209-3

Alignment_scores:
Quality: 1651.00 Length: 372
Ratio: 4.988 Gaps: 0
Percent Similarity: 88.978 Percent Identity: 76.075

Alignment_block:
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17 ePheLysLeuTTPGlyTTPThrMetLeuCysCysAspPheLeuAlaHis 34
156 CCGAAGCTGTGGCTCGACACTGCTGTTGTGACTTCCGATACACC 205
34 IseGlyThrTyrCysTTPThrTyrHisTyrSerGluLysProMetAsnTTP 50
206 ATGGAATCTACGTGTGGACTTACCATTTATCTGAAAACCCCATGACATG 255
51 GlnArgAlaArgArgPheCysArgAspAsnTyrThrAspLeuValAlaI 67
256 GAAATGTAGAAAGTTCTGCACAGCAAAATTCACAGATTAGTGCAT 305
67 eGlnAsnLysAlaGluIleGluTyrLeuGluLysThrLeuProPheSerA 84
306 ACAAAACAGAGAGAAATTCAGTATTAGACAAATACATTGCCCAAAAGCC 355
84 rGSetrTyrTTPrIleGlyIleArgLysIleGlyGlyIleTTPThrTTP 100

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356 356 CTAATTACTACTGATAGATGAGATCAGAGAAATTGGGAAATGTGGACATGG 405
101 101 ValGlyThrAsnLysSerLeuThrGluGluAlaGluAsnTrpPolYaspgI 117
406 406 GTGGAGAACCAACAAACACTCTCATTAAAGACAGACGAAGAACTGGGGTCTGG 455
117 117 ygluPProAsnAsnLysLysAsnLysGluAspCysValGluIleTyIle 134
456 456 GGAGGCCCAACAAAGAAAGTCCAAAGAGAGACTGTGTGGAGATCTAATATCA 505
134 134 ysATgAsnLysAspAlaGlyLysTrpAsnAspAspAlaGlyHisLysLeu 150
506 506 AGAGGGACGAGACTGTGGGAAATGGAAAGATGAGAGCCGTGTCAACAAACA 555
151 151 LysAlaAlaLeuCysTyTrpThrAlaSerCysGluProTrpSerCysSerGI 167
556 556 AAGGCACTCTCTGCTACACAGCCCTTTGGCCAGCCAGGCTTTGGCAATGG 605
167 167 yHISgLYGluCysValGluIleIleAsnAsnHisThrCysAsnCysAspY 184
606 606 CCGTGGAGAAATGTGTGCAAACTCAACAATCAACACAGTGCATCTGTGATG 655
184 184 aLgLYTyTrpGlyProGlnCysGluLeuValIleGlnCysGluProLeu 200
656 656 CAGGGATTTACGGGCCCCAGTGTCTGATGTGTGTCTCAGTGTAGCTTGTG 705
201 201 GluAlaProGluLeuGlyThrMetAspCysTrpHisProPheGlyAsnPh 217
706 706 GAGGCCCCGTGATGTGGGATGACATGAGACATGCATCCACCCCTTGGAAACTT 755
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756 756 CACCTTCACAGTCCAAAGTGTCTTCAACTGTCTTCAGGCAAGACAGACTAC 805
234 234 hrgLIleGluGluThrThrCysGlyProPheGlyAsnTrpSerPro 250
806 806 TTGGAGCTGCAGAAACACAGTGTGGAGCATCTGGAAACAGGTATCTCCA 855
251 251 GluProThrCysGluValIleGlnCysGluProLeuSerAlaProAspLe 267
856 856 GAGCCAACTCTGGCCAAAGTGTGCACAGTGTGAGCCCTTTGGAGCCCCGTGAGTT 905
267 267 uGlyIleMetAsnCysSerHisProLeuAlaSerPheSerPheTrpSerA 284
906 906 GGCTACCATGGAGACATCCACACCCCTTGGAAACTTCAGCTTCCAGTCCA 955
284 284 IacysTrpPheIleCysSerGlnGlyTrpGluLeuIleGlyLysLys 300
956 956 AGTGTGTCTTCAACTGTGTCTGAGGGAAGAGACTGTTGGAGCTGCAGAA 1005
301 301 ThrIleCysGluSerSerGlyIleTrpSerAsnProSerProIleCysGI 317
1006 1006 ACACAGATGTGGAGCATCTGGAAACTGTCATCTCCAGACCCCAATCTGGCCA 1055
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334 334 euPheIleProValAlaValMetValTrpAlaPheSerGlyLeuAlaPhe 350
1106 1106 TCTTCATCTCTGTAGCCGTCTGTGGTCAACGGCATTTCTGGGGGTGGCAVTT 1155
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; Sequence 2748, Application US/60230435
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; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NICOTIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO00768
; CURRENT APPLICATION NUMBER: US/60/230,435
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 2991
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2748
; LENGTH: 3238
; TYPE: DNA
; ORGANISM: HUMAN
US-60-230-435-2748

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56	eCySaIgaSPasntYrTrHrAspLeuAlaIleGlnAsnLysLaGIuI	73		
1865	CTCCCGGAGACAATTACACAGATTTCCTGCATACAAAAACCAAGCGCGAAA	1914		
73	legIuYrIleuGIuYsTrHrLeuProPheserAgssetYrTYrTriple	89		
1915	TTTAAGTATCTGGACAAAGACTCTGCCTTTTCACTCTTCTACTAGCATTA	1966		
90	GIuYrIleArGIuYsIleGIuYrIleTrpTrHrYpValGIyTrHrAsnLysSe	106		
1965	GGAAATCCGGAAGATAGAGAGAAATGTGACGCGGTGGGAAACCAACAATC	2014		
106	rIeuYrHrGIuYsIleAlaIleAsnTrpGIuYsArgIuYsLProAsnAsnLysL	123		
2015	TTCTTACTGAGAAAGCAGAGAAGCTGGGAGATGTGGACCCCAACAACAGA	2064		
123	ysAsnLysGIuAspCyValGIuYrIleYrIleYsArGAsnLysAspAla	139		
2065	AGAACAAAGGAGGACTGGCTGGAGATCTATATCAAGACAGAAACAAAGATGCA	2114		
140	GIuYsTrpAsnAspAspAlaCyHnIysLysLeuLysAlaIleLeuCyTy	156		
2115	GGCAAAATGGAACGATGACGCTGCCAACAACTAAAGCAGCGCTCTGTTA	2164		
156	rTrpAlaIaser.....CysGIuProTrpSerCysSerGIyHnIleGIuYs	171		
2165	CACAGCTAGGACGACTGACAAACAGCGCTATGCGCTCCGAGACTCAGCAAGGG	2214		
171	ysValGIuIleIleAsnAsnHnIstHrCyAsnCyAspValGIuYrTYr	187		
2215	CCACG.....ATCAAAATATTACACCTGCACAACTGTGATGTGGGTACAT	2258		
188	GIYrProGIuYsGln.....LeuValIleClnIcYsGIuProLe	200		
2259	GGGCCCCAGGTGATGTGGTAAAGTCTCTTCTTCTTTGGCTCTCTCTT	2308		
200	uGIuAlaProGIuYsLcYrHnIleTasArCySTrHnIstProheGIuYsP	217		
2309	AGGTAAA.....CTCACAGGAATACACTCACCCCTTTGGGAAACT	2346		
217	heserPheserSerGIuYsAlaPheserCysSerGIuYrIleHrAsnLeu	233		

```
|||||
2347 TCAGCTTCAGCTCACAGTGTGCTTCAGCTCTCGAAGGAACAACCTTA 2396
234 ThrGlyIleGluGluThrThrCysGlyProPheGlyAsnTrpSerSerPr 250
|||||
2397 ACTGGGATTGAAGAAACCACCTGTGGACATTGGAAACGTGGTCATCTCC 2446
250 OGluProThrCysGluVal.....IleGluCysGluProLeuSerAlap 265
|||||
2447 AGAACCAACCTGTCAGGTGAGTAACCTCAGACTAGAGGTTTGTGTCATGC 2496
265 roAspLeuGlyIleMetAsnCysSerHisProLeuAlaSerPheSerPhe 281
|||||
2497 AATACCTGGGCTTACAG.....AGCCATCCCTGGCCAGCTTCAGCTTT 2540
282 ThrSerAlaCysThrPheIleCysSerGluGlyThrGluLeuIleGlyLy 298
|||||
2541 ACCTCTGCATGTACCTTCATCTGCTCGAAGAACTGATTAAATGGGAA 2590
298 sLysLyThrIleCysGluSerSerGlyIleTrpSerAsnProSerProI 315
|||||
2591 GAAGAAACCACTTGTGAATCATCTGGAATCTGTCAAATCTAGTCCAA 2640
315 IeCysGluLysLeuAspLysSerPheSerMetIleLysGluGlyAspTyr 331
|||||
2641 TATGTCAAAGTGAGTAAGTTGTCTCGAAGAACTGAAATCTTAACGATGG 2690
332 AsnProLeuPheIleProValAlaValMetValThrAlaPheSerGlyLe 348
|||
2691 AGCTGATGTTTCATTCACGTGCGCAGTCACTGATCTGCAATCTCTGGGTT 2740
348 uAlaPheIleIleTrpLeuAlaArgArgLeuLysLyGly 361
|||||
2741 GGCATTTATCATTTGGCTGCGCAGGAGATTAAAAAAGGT 2780
```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 12, 2001, 21:40:24 ; Search time 70.99 seconds

(without alignments)
355.811 Million cell updates/sec

Title: US-09-119-209-2

Perfect score: 2116

Sequence: 1 MIFPWKCSTORDLNMIFKL.....WLARRLKGGKSKSRMNDPY 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: PIR.66:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2090	98.8	385	1 A34015	L-selectin precurs
2	1992	94.1	372	2 JC5377	L-selectin precurs
3	1796	84.9	376	2 JC4892	L-selectin precurs
4	1682	79.5	370	2 S22124	L-selectin precurs
5	1653	78.1	372	2 S23936	L-selectin precurs
6	1652	78.1	372	1 S09702	L-selectin precurs
7	1651	78.0	372	1 A32375	L-selectin precurs
8	905	42.8	830	2 A30359	P-selectin precurs
9	902.5	42.7	768	2 A42755	P-selectin precurs
10	894.5	42.3	646	2 JN0473	P-selectin precurs
11	885	40.7	768	2 I53821	P-selectin - rat
12	862	40.7	610	2 A35046	E-selectin precurs
13	861	40.7	551	2 I46709	endothelial leukoc
14	857	40.5	612	2 S23174	endothelial leukoc
15	857	40.5	618	2 B42755	E-selectin precurs
16	849.5	40.1	485	2 S36772	E-selectin - bovin
17	815.5	38.5	482	2 JC5092	E-selectin - pig
18	236	11.2	868	2 T20239	hypothetical prote
19	212.5	10.0	473	2 B38738	coagulation factor
20	212.5	10.0	1019	2 A38738	coagulation factor
21	199.5	9.4	449	1 NBH0HS	complement factor
22	199.5	9.4	1231	1 NBH0HS	complement factor
23	175.5	8.3	2014	2 I36936	complement recepto
24	172	8.1	2489	2 I73012	complement C3b/C4b
25	171.5	8.1	597	1 S53711	C4b alpha chain p
26	170	8.0	404	2 A46274	HIV gp120-binding
27	168	7.9	2132	1 A55182	aggreccan precursor
28	167	7.9	321	1 LNM0ER	IgE Fc receptor II
29	167	7.9	1234	1 NBMSH	complement factor

30	166.5	7.9	558	2 S57953	C4b protein alpha
31	166	7.8	1456	1 A36563	mannose receptor p
32	165.5	7.8	560	2 T16833	hypothetical prote
33	165.5	7.8	1479	2 T42710	mannose receptor,
34	165	7.8	311	1 LNM02A	asialoglycoprotein
35	164.5	7.8	482	2 A34924	complement C3b/C4b
36	163	7.7	669	2 S65551	factor II - bovine
37	163	7.7	2124	2 A28452	proteoglycan core
38	162.5	7.7	345	1 NBBO	apolipoprotein H p
39	162	7.7	304	2 JX0209	lectin, galactose/
40	162	7.7	600	2 S62786	aggreccan - human
41	162	7.7	1574	2 T13954	MEGF6 protein - ra
42	161	7.6	469	1 NBMSC4	C4b-binding protei
43	160.5	7.6	1455	1 A48925	mannose receptor p
44	160	7.6	638	2 S08042	proteoglycan core
45	160	7.6	1091	1 PL0009	complement C3d/Eps

ALIGNMENTS

RESULT 1
A34015
L-selectin precursor, long splice form - human
N:Alternate names: CD62L; leucocyte cell adhesion molecule-1 (LECAM-1, LAM-1); leukoc
ral lymph node homing receptor Leu-8
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: I55333; S06798; JLO104; A34015; A33912
R:Ord, D.C.; Ernst, T.J.; Zhou, L.J.; Rambaldi, A.; Spertini, O.; Griffin, J.; Tedder
J. Biol. Chem. 265, 7760-7767, 1990
A:Title: Structure of the gene encoding the human leukocyte adhesion molecule-1 (TQ1,
A:Reference number: I55333; MUID:90243637
A:Accession: I55333
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 14-385 <CND>
A:Cross-references: GB:M32414; NID:q187259; PIDN:AMB60700.1; PID:g386860
R:Cametini, D.; James, S.P.; Stamenkovic, I.; Seed, B.
Nature 342, 78-82, 1989
A:Title: Leu-8/TQ1 is the human equivalent of the Mel-14 lymph node homing receptor.
A:Reference number: S06798; MUID:90044046
A:Accession: S06798
A:Molecule type: mRNA
A:Residues: 1-225, 'S', 227-385 <CAM>
A:Cross-references: EMBL:X17519; NID:g34344; PIDN:CA843536.1; PID:g4902829
A:Note: this translation is not annotated in GenBank entry HSL808, release 111.0
R:Redder, T.F.; Isaacs, C.M.; Ernst, T.J.; Demetri, G.D.; Adler, D.A.; Distche, C.N.
J. Exp. Med. 170, 123-133, 1989
A:Title: Isolation and chromosomal localization of cDNAs encoding a novel human lymph
oetins.
A:Reference number: JLO104; MUID:89310350
A:Accession: JLO104
A:Molecule type: mRNA
A:Residues: 1-230, 'N', 232, 'N', 234-254, 'E', 256-385 <TED>
A:Cross-references: GB:X16150; NID:g34428; PIDN:CA8434275.1; PID:g34429
A:Note: the translated sequence in GenBank entry HSLVMI, release 111.0, differs from
R:Bowen, B.R.; Nguyen, T.; Laskey, L.A.
J. Cell Biol. 109, 421-427, 1989
A:Title: Characterization of a human homologue of the murine peripheral lymph node ho
A:Reference number: A34015; MUID:89308881
A:Accession: A34015
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 14-49, 'Y', 51-190, 'H', 192-205, 'L', 207-226, 'F', 228-385 <BOW>
A:Cross-references: GB:X16070; NID:g38092; PIDN:CA8434203.1; PID:g38093
R:Sieglman, M.H.; Weisman, I.L.
Proc. Natl. Acad. Sci. U.S.A. 86, 5562-5566, 1989
A:Title: Human homologue of mouse lymph node homing receptor: evolutionary conservati
A:Reference number: A33912; MUID:89315837
A:Accession: A33912
A>Status: preliminary
A:Molecule type: mRNA

A:Residues: 14-205, L', 207-385 <SITE>
 A:Cross-References: GB:M25280; NID:9187182; PIDN:AAC63053.1; PID:9307134
 C:Comment: For an alternative splice form, see PIR:S09702.
 C:Genetics:
 A:Gene: GDB:SELL; GDB:LNHR; LSEL; LAM1; LYAM1; LAM-1
 A:Cross-References: GDB:120157; GDB:118834; OMIM:153240
 A:Map position: 1q22-1q23
 A:Insertions: 14/3; 42/1; 171/1; 207/1; 269/1; 331/1; 374/1; 380/2
 C:Function:
 A:Description: binds with low affinity to oligosaccharides like heparan sulfate and sialy
 ment of leucocytes to areas of inflammation, and with CD162 mediates neutrophil-neutroph
 C:Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homology
 C:Keywords: alternative splicing; cell adhesion; duplication; glycoprotein; inflammation
 F:1-51/Domain: signal sequence #status predicted <SIG>
 F:42-168/Domain: C-type lectin homology <LCH>
 F:52-385/Product: L-selectin #status predicted <MNT>
 F:52-343/Domain: extracellular #status predicted <EXT>
 F:173-204/Domain: EGF homology <EGF>
 F:210-267/Domain: complement factor H repeat homology <FHH1>
 F:272-329/Domain: complement factor H repeat homology <FHH2>
 F:344-368/Domain: transmembrane #status predicted <TM>
 F:369-385/Domain: intracellular #status predicted <INT>
 F:73,117,190,245,259/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:377,380/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 98.8%; Score 2090; DB 1; Length 385;
 Best Local Similarity 98.9%; Pred. No. 5,6e-148;
 Matches 368; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY	1	MIFPMKCGSTORDLNNIFKLMGWTMLCCDFLAHNGTCWTHYSEKPMNMORARRPCRDN	60
DB	14	MIFPMKCGSTORDLNNIFKLMGWTMLCCDFLAHNGTCWTHYSEKPMNMORARRPCRDN	73
QY	61	YTDLVAIONKAEIEYLEKTLPEFSRSYWIIGIRKIGITWVGINSLTREAEENMGDGEFN	120
DB	74	YTDLVAIONKAEIEYLEKTLPEFSRSYWIIGIRKIGITWVGINSLTREAEENMGDGEFN	133
QY	121	NKKNKEDCEVEIYIKRNKAGKNDACCHKLAALCYTASCPWSSGSGEGCEVEITNNHTC	180
DB	134	NKKNKEDCEVEIYIKRNKAGKNDACCHKLAALCYTASCPWSSGSGEGCEVEITNNHTC	193
QY	181	NCVGVYGGPOQVLYICEPLAEPLGTMDCTHPFGNFSFSQCAFSCSEGTNLGIEETT	240
DB	194	NCVGVYGGPOQVLYICEPLAEPLGTMDCTHPFGNFSFSQCAFSCSEGTNLGIEETT	253
QY	241	CGPFGNMSSPEPTCOVIOCEPLASAPDLGIMNCSHPLASFSTSACTFCSEGTTELIGKK	300
DB	254	CGPFGNMSSPEPTCOVIOCEPLASAPDLGIMNCSHPLASFSTSACTFCSEGTTELIGKK	313
QY	301	TICSSSGIWSNPSPICQKLDKSFMSIKESDPNPLFTPAVAVMTAFSGLAFTIIMLARLKK	360
DB	314	TICSSSGIWSNPSPICQKLDKSFMSIKESDPNPLFTPAVAVMTAFSGLAFTIIMLARLKK	373
QY	361	GKSKSRSMNDPY 372	
DB	374	GKSKSRSMNDPY 385	

RESULT 2
 JC5377
 L-selectin precursor - hamadryas baboon
 C:Species: Papio hamadryas (hamadryas baboon)
 C:Date: 02-Jun-1997 #sequence_revision 12-Sep-1997 #text_change 21-Jan-2000
 C:Accession: JC5377; PC4315
 R:Tsunashita, N.; Fu, H.; Berg, E.L.
 A:Title: PCR cloning of the cDNA encoding baboon L-selectin.
 A:Reference number: JC5377; MUID:97128794
 A:Accession: JC5377
 A:Molecule type: mRNA
 A:Residues: 1-372 <TSU1>
 A:Cross-References: GB:U52074; NID:91326148; PIDN:AAB40903.1; PID:91326149

A:Accession: PC4315
 A:Molecule type: protein
 A:Residues: 37-43;142-148 <TSU2>
 C:Comment: This receptor is involved in the initial adhesive interaction between lymph
 sites of inflammation.
 C:Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homology
 F:1-38/Domain: signal sequence #status predicted <SIG>
 F:138-155/Domain: C-type lectin homology <LCH>
 F:339-372/Product: L-selectin #status predicted <MNT>
 F:39-157/Domain: calcium-binding #status predicted <CAB>
 F:160-191/Domain: EGF homology <EGF>
 F:197-254/Domain: complement factor H repeat homology <FHH1>
 F:259-316/Domain: complement factor H repeat homology <FHH2>
 F:333-355/Domain: transmembrane #status predicted <TM>
 F:356-372/Domain: intracellular #status predicted <INT>

Query Match 94.1%; Score 1992; DB 2; Length 372;
 Best Local Similarity 93.5%; Pred. No. 1e-140;
 Matches 348; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY	1	MIFPMKCGSTORDLNNIFKLMGWTMLCCDFLAHNGTCWTHYSEKPMNMORARRPCRDN	60
DB	1	MIFPMKCGSTORDLNNIFKLMGWTMLCCDFLAHNGTCWTHYSEKPMNMORARRPCRDN	60
QY	61	YTDLVAIONKAEIEYLEKTLPEFSRSYWIIGIRKIGITWVGINSLTREAEENMGDGEFN	120
DB	61	YTDLVAIONKAEIEYLEKTLPEFSRSYWIIGIRKIGITWVGINSLTREAEENMGDGEFN	120
QY	121	NKKNKEDCEVEIYIKRNKAGKNDACCHKLAALCYTASCPWSSGSGEGCEVEITNNHTC	180
DB	121	NKKNKEDCEVEIYIKRNKAGKNDACCHKLAALCYTASCPWSSGSGEGCEVEITNNHTC	180
QY	181	NCVGVYGGPOQVLYICEPLAEPLGTMDCTHPFGNFSFSQCAFSCSEGTNLGIEETT	240
DB	181	NCVGVYGGPOQVLYICEPLAEPLGTMDCTHPFGNFSFSQCAFSCSEGTNLGIEETT	240
QY	241	CGPFGNMSSPEPTCOVIOCEPLASAPDLGIMNCSHPLASFSTSACTFCSEGTTELIGKK	300
DB	241	CGPFGNMSSPEPTCOVIOCEPLASAPDLGIMNCSHPLASFSTSACTFCSEGTTELIGKK	300
QY	301	TICSSSGIWSNPSPICQKLDKSFMSIKESDPNPLFTPAVAVMTAFSGLAFTIIMLARLKK	360
DB	301	TICSSSGIWSNPSPICQKLDKSFMSIKESDPNPLFTPAVAVMTAFSGLAFTIIMLARLKK	360
QY	361	GKSKSRSMNDPY 372	
DB	361	GKSKSRSMNDPY 372	

RESULT 3
 JC4892
 L-selectin precursor - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 21-Jan-2000
 C:Accession: JC4892
 R:Qian, J.; Huang, X.; Marks, R.M.
 Biochem. Biophys. Res. Commun. 225, 406-412, 1996
 A:Title: Cloning of the cDNA for rabbit L-selectin and expression of recombinant prot
 A:Reference number: JC4892; MUID:96354800
 A:Accession: JC4892
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-376 <QIA>
 A:Cross-References: GB:U26535; NID:9847787; PIDN:AAA67896.1; PID:9847788
 C:Comment: This protein involved in leukocyte-endothelial adhesion; it mediates adhes
 C:Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homology
 F:29-155/Domain: signal sequence #status predicted <SIG>
 F:38-376/Product: L-selectin #status predicted <LCH>
 F:160-191/Domain: EGF homology <EGF>
 F:197-254/Domain: complement factor H repeat homology <FHH1>
 F:259-316/Domain: complement factor H repeat homology <FHH2>

```

Query Match 84.9%: Score 1796; DB 2; Length 376;
Best Local Similarity 84.1%: Pred. No. 3,6e-126;
Matches 311; Conservative 24; Mismatches 35; Indels 0; Gaps 0;

Oy 1 MIFPKKCOSTOPDLNIFKLMGWTMLCCDFLAHHCYTCWYHYSEKPMNQARARFCRDN 60
Db 1 MIFPKKCOPOGLNINVFLLMWTATLCCDFLAHGNICWYHYSEKPMNERARKFCRDN 60
Oy 61 YTDLVAIQNKAEIYLEKTLTPFSRSYWIIGIRKIGITWTVGINKSLTEBAENMGDEPN 120
Db 61 YTDLVAIQNKGEIYLEKTLTPFSRSYWIIGIRKIGITWTVGINKSLTEBAENMGDEPN 120
Oy 121 MKKNNEDCEYIITKRRKDKAGKNNDDACIKLKAALCTTASQPMSCSGHGCEVELINNHTC 180
Db 121 MKKTEDCEYIITKRLRDSKGNDDSCORRKALCTTASCHPGSCSHGCEVINYTC 180
Oy 181 NCDVGYVGGQCOLVIOCEPLLEAPELCTMDCTHPFGNMFSPSGCAFSCSEGTNLGIEET 240
Db 181 SCDVGYVGGQCOLVIOCEPLLEAPELCTMDCTHPFGNMFSPSGCAFSCSEGTNLGIEET 240
Oy 241 CGPFGNMSPEPTCOYIOCEPLSAPDLGIMNCSHPLASFTSACTFTICEGTELGKKR 300
Db 241 CGPLGNMSLRLPTCOYIOCEPLTAPDLGTDCSHPRAVFGFTSTCFPSCEGALLGKKR 300
Oy 301 TTCSSGIMTNSNPICQIKDKSFSMIKEGDYNFLFPVAVMTAFSGLATIIMLARLKK 360
Db 301 TVCGSSGIMSSPTPKQKVDKRSFSMIKEGDYNFLFPVAVMTAFSGLATIIMLARLKK 360
Oy 361 GKSKRSKMD 370
Db 361 GKSKRSKDD 370

RESULT 4
S22124
L-selectin precursor - bovine
N:Alternate names: Leucocyte cell adhesion molecule 1 (LECAM-1)
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #lex_change 21-Jan-2000
C:Accession: S22124; A46531
R:Bosworth, B. Jr.
submitted to the EMBL Data Library, October 1991
A:Reference number: S22123
A:Accession: S22124
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-370 <BOS>
A:Cross-references: EMBL:X62882; NID:9515; PID:CA44676.1; PID:9516
R:Walcheck, B.; White, M.; Kurk, S.; Kishimoto, T.K.; Jutila, M.A.
Eur. J. Immunol. 22, 469-476, 1992
A:Title: Characterization of the bovine peripheral lymph node homing receptor: a lectin
A:Reference number: A46531; MUID:92164727
A:Accession: A46531
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 39-79, 'Q', 81-151, 'K' <MAL>
A:Note: sequence inconsistent with the nucleotide translation
C:Superfamily: L-selectin, C-type lectin homology (NCBIN:85686, NCARP:85687)
F:29-155/Domain: C-type lectin homology <LCH>
F:160-191/Domain: EGF homology <EGF>
F:197-254/Domain: complement factor H repeat homology <FH1>
F:259-316/Domain: complement factor H repeat homology <FH2>

Query Match 79.5%: Score 1682; DB 2; Length 370;
Best Local Similarity 77.0%: Pred. No. 1e-117;
Matches 282; Conservative 42; Mismatches 40; Indels 2; Gaps 1;

Oy 1 MIFPKKCOSTOPDLNIFKLMGWTMLCCDFLAHHCYTCWYHYSEKPMNQARARFCRDN 60
Db 1 MIFPKKCOPOGLNINVFLLMWTATLCCDFLAHGNICWYHYSEKPMNERARKFCRDN 60

```

Db 1 MLCRKCQNAQGLMNVKELMWIMLCDDFAFHGHTDCMTHYKSRPRPWKARAFCHEN 60

QY 61 YTDLVAIONKAEIEYLEKTLTPFSRSYWIIGIRKIGCIGTWGTNKSLTLEAEENMGDGEPN 120

Db 61 YTDLVAIONKGEIEINTKTLTPFSRTYWIIGIRKVEGVMTWGTNKSLTLEAEENMGAGEPN 120

QY 121 NKKNKEDVEEYIKRNNKAGKWNDDACHKLAALCYTASQCPWSSGSGEGVEIINNNTC 180

Db 121 NKKRSDEVEYIKRNNKSGKWNDDACHKATATLCYTASCKPWSGSGGQCEVYINNNTC 180

QY 181 NCDVAYYPCQOLVYQCEPLLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLGTIEETT 240

Db 181 NCDLGYTEPCQFVYQCPLEAPRLCTHACCHPLCNFSFMSQACAFNCCKGIDMIGVEETT 240

QY 241 CGPFGNWSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSFTSACTFTCSGTELGIRKK 300

Db 241 CAPFNMSSEPTCHVIOCEPLTEPDLGTMDCNHPLVDYDFGFSSTCTFCSEDEALTEGKK 300

QY 301 TICESSGTMSNPICQKLDKFSMIKEGDYNPFLIPAAVWYTAISGLAFIIMLARLKK 360

Db 301 TICGLSGMWSPEPCQKINRTISINESDYNPFLIPAAVWYTAISGLAFIIMLARLK- 359

QY 361 GKSKR 366

Db 360 -RKSKK 364

RESULT 5

S23936

L-selectin precursor - rat

N:Alternate names: leucocyte cell adhesion molecule 1 (LECAM-1)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 20-Jun-2000

C:Accession: S23936

R:Manabe, T.; Song, Y.; Hirayama, Y.; Tamatani, T.; Kuida, K.; Miyasaka, M. Biochim. Biophys. Acta 1131, 321-324, 1992

A:Title: Sequence and expression of a rat cDNA for LECAM-1.

A:Reference number: S23936; MUID:92329548

A:Accession: S23936

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-372 <MAN>

A:Cross-references: GB:D10831; NID:g220801; PIDN:BA01613.1; PID:g220802

C:Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homology

C:Keywords: transmembrane protein

F:29-155/Domain: C-type lectin homology <LCH>

F:160-191/Domain: EGF homology <EGF>

F:197-254/Domain: complement factor H repeat homology <FH>

F:259-316/Domain: complement factor H repeat homology <FH2>

Query Match 78.1%; Score 1653; DB 2; Length 372;

Best Local Similarity 76.9%; Pred. No. 1.5e-115;

Matches 286; Conservative 35; Mismatches 51; Indels 0; Gaps 0;

QY 1 MIFPKCOSTORDIMNIFKLMGWTMLCCDPLAHNGTCMYHYSEKPMNMQRARFCRDN 60

Db 1 MYEPRCQSAQSGMSFLKMLIRTLCCDLLPHGTHCMTYHYSRSMNWNENARFCFHN 60

QY 61 YTDLVAIONKAEIEYLEKTLTPFSRSYWIIGIRKIGCIGTWGTNKSLTLEAEENMGDGEPN 120

Db 61 YTDLVAIONKREIEYLEKTLTPKNPYYWIGIRKIGKTTWGTNKTLEAEENMGCTGEPN 120

QY 121 NKKNKEDVEEYIKRNNKAGKWNDDACHKLAALCYTASQCPWSSGSGEGVEIINNNTC 180

Db 121 NKKRSDEVEYIKRNNKSGKWNDDACHKRAALCYTASQCESCNRRGECVEIINNNTC 180

QY 181 NCDVAYYPCQOLVYQCEPLLEAPELGTMDCTHPFGNFSFSSQCAFSCSEGTNLGTIEETT 240

Db 181 ICDEPYVYQCGOYVYQCEPLKAPELGTMCNCHPLGDSFQSCAFNCSEGSSELGMAKTE 240

QY 241 CGPFGNWSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSFTSACTFTCSGTELGIRKK 300

Db 241 CGPFGNWSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSFTSACTFTCSGTELGIRKK 300

||||| 61 YTDLAIQNKKEIELEFTLPKSPYYWIGIRKIGKMTWTWGTNTLTKEAENMGAGEPN 120
QY 121 NKKNKEDVEIYIRKRNKDGAKMNDACHKLAALCYTASCOPMSCSGHECEVEIINNHTC 180
Db 121 NKKKEDVEIYIRKRNKDGAKMNDACHKRAALCYTASCOPMSCSGNGGECVEIINNHTC 180
QY 181 NCDVGYTGPOQOLVIOCEPLEAPELGTMDCTHPFGNFSFSQCAFSCSEGTNLGIEETT 240
Db 181 ICDVGYTGPOQOLVIOCEPLEAPELGTMDCTHPFGNFSFSQCAFSCSEGTNLGIEETT 240
QY 241 CGPFGNMSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTISACTFICSSEGTILGKKK 300
Db 241 CGASGMNSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTISACTFICSSEGTILGTAE 300
QY 301 TTCSSGTWSPICOKLDFKSMIRKEDYNPLETIPAAVWVTAFAAGTIFIMLARLKK 360
Db 301 TQCGASGMNSPEPTCOETNFSFKIRKEDYNPLETIPAAVWVTAFAAGTIFIMLARLKK 360
QY 361 GKSKRSMDPY 372
Db 361 GKSKRMDPY 372

RESULT 8
A30359
P-selectin precursor - human
N:Alternate names: CD62 antigen; granule membrane protein 140
C:Species: Homo sapiens (man)
C:Date: 18-Oct-1989 #sequence_rev1sion 30-Sep-1991 #text_change 19-May-2000
C:Accession: A30359
R:Johnston, G.I.; Cook, R.G.; McEver, R.P.
Cell 56, 1033-1044, 1989
A:Title: Cloning of GMP-140, a granule membrane protein of platelets and endothelium: se
A:Reference number: A30359; MUID:89166432
A:Accession: A30359
A:Molecule type: mRNA
A:Residues: 1-830 <JOH>
A:Cross-references: GB:M25322
A>Note: parts of this sequence, including the amino end of the mature protein, were cont
A:Gene: GDB:SELP; GRMP
A:Cross-references: GDB:120018; OMIM:173610
A:Map position: 1q22-1q25
C:Superfamily: unassigned EGF-related proteins; complement factor H repeat homology; EGF
C:Keywords: cell adhesion; glycoprotein; phosphohistidine; phosphoprotein; surface anti
F:1-41/Domain: signal sequence #status predicted <SIG>
F:42-830/Product: P-selectin #status experimental <MAT>
F:163-194/Domain: EGF homology <EGF>
F:200-257/Domain: complement factor H repeat homology <FHO1>
F:262-319/Domain: complement factor H repeat homology <FHO2>
F:324-381/Domain: complement factor H repeat homology <FHO3>
F:386-443/Domain: complement factor H repeat homology <FHO4>
F:448-505/Domain: complement factor H repeat homology <FHO5>
F:510-567/Domain: complement factor H repeat homology <FHO6>
F:572-629/Domain: complement factor H repeat homology <FHO7>
F:642-699/Domain: complement factor H repeat homology <FHO8>
F:704-761/Domain: complement factor H repeat homology <FHO9>
F:772-795/Domain: complement factor H repeat homology <FHO9>
F:796-830/Domain: transmembrane #status predicted <TM>
F:54,98,180,212,219,411,460,518,665,716,723,741/Binding site: carbohydrate (Asn) (cova

Query Match 42.8%; Score 905; DB 2; Length 830;
Best Local Similarity 50.6%; Pred. No. 1,1e-59;
Matches 157; Conservative 47; Mismatches 106; Indels 0; Gaps 0;
QY 8 OSTRODLNMTIKMGWMLCCDFLAHHGTYCMTYHSEKPMNQARARFCRDNTDLVAI 67
Db 11 QREGRVYVFGISQLCFSLSELNKEVAAWYTHYSKAVSMISRKVCNRTDLVAI 70
QY 68 QNKAIEYLEKTELPFSRSYYWIGIRKIGTITWVTGNTSLTEAEENMGDEPNKKKED 127

Db 71 QNKNEIDYLNKVLPPYSSYYWIGIRKNNKMTWGTGKALNLNEAENMADNEPNKRNED 130
QY 128 CVEIYIKRNKDGAKMNDACHKLAALCYTASCOPMSCSGHECEVEIINNHTCNDVGY 187
Db 131 CVEIYIKRSPASAGKMNDRHCLKKHALCYTASCOPMSCSGKQCELEFIGNYKCSCTPEFY 190
QY 188 GPQOLVIOCEPLEAPELGTMDCTHPFGNFSFSQCAFSCSEGTNLGIEETTGPFGNW 247
Db 191 GPECEYRECEGELPQVHVLNMCNSHPLCNFSPNSQCSFHCFTDGVNPSKLECLASGIW 250
QY 248 SSPPTCOVIOCEPLSAPDLGIMNCSHPLASFSTISACTFICSSEGTILGKKKTCSSG 307
Db 251 TNKPQCLAACCPPLKIPERGNMTCLSAKAFQHQSSCSFSCSEGFALVGEVWQCTASG 310
QY 308 IWSNPSICO 317
Db 311 VWTAPAPYCK 320

RESULT 9
A42755
P-selectin precursor - mouse
N:Alternate names: CD62; granule membrane protein 140; PADGEM
C:Species: Mus musculus (house mouse)
C:Date: 04-Mar-1993 #sequence_rev1sion 18-Nov-1994 #text_change 19-May-2000
C:Accession: A42755; A44899
R:Weller, A.; Isenmann, S.; Vestweber, D.
J. Biol. Chem. 267, 15176-15183, 1992
A:Title: Cloning of the mouse endothelial selectins. Expression of both E- and P-sele
A:Reference number: A42755; MUID:92340571
A:Accession: A42755
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-768 <WEL>
A:Cross-references: GB:M87861; NID:g200552; PIDN:AAA40008.1; PID:g200553
A:Experimental source: endothelial cells
A>Note: sequence extracted from NCBI backbone (NCBI:P:109467)
R:Sanders, W.E.; Wilson, R.W.; Ballantyne, C.M.; Beaudet, A.L.
Blood 80, 795-800, 1992
A:Title: Molecular cloning and analysis of in vivo expression of murine P-selectin.
A:Reference number: A44899; MUID:92345617
A:Accession: A44899
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-723, 'F', 725-768 <SAN>
A:Cross-references: GB:M72332; NID:g193565; PIDN:AAA37712.1; PID:g193566
A>Note: sequence extracted from NCBI backbone (NCBI:P:109900)
C:Superfamily: unassigned EGF-related proteins; complement factor H repeat homology;
C:Keywords: cell adhesion; glycoprotein; phosphohistidine; phosphoprotein; transmembr
F:1-41/Domain: signal sequence #status predicted <SIG>
F:42-768/Product: P-selectin #status predicted <MAT>
F:163-194/Domain: EGF homology <EGF>
F:200-257/Domain: complement factor H repeat homology <FHO1>
F:262-319/Domain: complement factor H repeat homology <FHO2>
F:324-381/Domain: complement factor H repeat homology <FHO3>
F:386-443/Domain: complement factor H repeat homology <FHO4>
F:448-505/Domain: complement factor H repeat homology <FHO5>
F:510-567/Domain: complement factor H repeat homology <FHO6>
F:580-637/Domain: complement factor H repeat homology <FHO7>
F:642-699/Domain: complement factor H repeat homology <FHO8>
F:710-733/Domain: transmembrane #status predicted <TM>
F:734-768/Domain: intracellular #status predicted <INT>
F:45,54,107,212,347,398,456,467,603,654,661,679/Binding site: carbohydrate (Asn) (cov

Query Match 42.7%; Score 902.5; DB 2; Length 768;
Best Local Similarity 52.0%; Pred. No. 1,6e-59;
Matches 156; Conservative 40; Mismatches 103; Indels 1; Gaps 1;
QY 20 LMGWMLCCDFLAHHGTYCMTYHSEKPMNQARARFCRDNTDLVAIONKAIEYLEKT 79
Db 24 IWFSLISELVNKEVAAWYNTSKAYSWNNSRVERCRHFTDLVAIONKNEIHLMDV 82

[illegible]

Proc. Natl. Acad. Sci. U.S.A. 87, 1673-1677, 1990

Leukocyte adhesion molecule 1: direct expression cloning and function

A:Reference number: A35046; MUID:90175359
A:Accession: A35046
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-610 <HESS>
R:Cross-references: GB:A30640; NID:g182047; PIDN:AA52377.1; PID:g182048
R:Bivellacqua, M.P.; Stengelin, S.; Gmbrore Jr., M.A.; Seed, B.
Science 243, 1160-1165, 1989
A:Title: Endothelial leukocyte adhesion molecule 1: an inducible receptor for neutrophils
A:Reference number: A32606; MUID:89162047
A:Accession: A32606
A:Molecule type: mRNA
A:Residues: 1-467, 'Y', 469-610 <BEV>
R:Cross-references: GB:M24136; NID:g537523; PIDN:AA52376.1; PID:g537524
C:Genetics:
A:Gene: GDB:SELE; ELAM; ESEL; ELAM1
A:Cross-references: GDB:120612; OMIM:131210
A:Map position: 1q22-1q25
C:Superfamily: unassigned EGF-related proteins; C-type lectin homology; complement factor
C:Keywords: duplication; glycoprotein; tandem repeat; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:12-138/Domain: C-type lectin homology <LCH>
F:22-610/Product: endothelial leukocyte adhesion molecule 1 #status predicted <MAT>
F:143-174/Domain: EGF homology <EGG>
F:180-237/Domain: complement factor H repeat homology <HN01>
F:242-299/Domain: complement factor H repeat homology <HN02>
F:304-362/Domain: complement factor H repeat homology <HN03>
F:367-425/Domain: complement factor H repeat homology <HN04>
F:430-488/Domain: complement factor H repeat homology <HN05>
F:493-547/Domain: complement factor H repeat homology <HN06>
F:557-578/Domain: transmembrane #status predicted <TMW>
F:253,145,160,179,199,203,265,312,332,503,527/Binding site: carbohydrate (Asn) (covalently

QY 270 MNCSHPLASFSTSACTFICSECTELIGKKKTTICSSGIWSPSPICQ 317
 11 : : : 111 11 : : 11111 : : :
 Db 261 RKCSSNPGSYFWNTTCTCFDCVEGYRRVGAQNLQCTSSSGIWDNETPSCK 308

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QY      2/0  MNC SHPLASFSITSACTFICSEGTFLGKKKKTICSSSGIWSNPSPIQ  317
          ||  | : : ||| | | | : : | |||| | : | :
Db      254  RKCSSNPGSYPWNTTCTFDCVEGIYRVGAQNLQCTSSGIWDNETPSC  301

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B42755

Query Match	40.5%;	Score 857;	DB 2;	Length 618;
Best Local Similarity	51.4%;	Pred. No. 3e-56;		
Matches 148;	Conservative 42;	Mismatches 96;	Indels 2;	Gaps 2

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QY      211 THPGNFSFSSQCFAFCSEGTNLTGIEET- CGPFGNSSPEPTCQVIOCEPLSADLGI    269  
        :||| ||:::|| |   ::|| |   ||| |||::||| |||::||  
Db       201 SHPGPSYSNSCSFGCKRGYLPSMETIVRCTSSGEASAPAPACHVEECALTHAHGI    260
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 13, 2001, 01:14:47 ; Search time 32.92 Seconds

(without alignments)
364.927 Million cell updates/sec

Title: US-09-119-209-2

Perfect score: 2116

Sequence: 1 MIPMKCOSTORDLNMIFKL.....MLARRLKKGKSKRSMNDPY 372

Scoring table: HLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	2090	98.8	372 1	LEM1_HUMAN
2	2085	98.5	372 1	LEM1_PANTR
3	2062	97.4	372 1	LEM1_PONPY
4	1996	94.3	372 1	LEM1_MACMU
5	1992	94.1	372 1	LEM1_PAPHA
6	1682	79.5	370 1	LEM1_BOVIN
7	1653	78.1	372 1	LEM1_RAT
8	1651	78.0	372 1	LEM1_MOUSE
9	919.5	43.5	769 1	LEM3_SHEEP
10	905	42.8	830 1	LEM3_HUMAN
11	902.5	42.7	768 1	LEM3_MOUSE
12	894.5	42.3	646 1	LEM3_BOVIN
13	885	41.8	768 1	LEM3_RAT
14	862	40.7	610 1	LEM2_HUMAN
15	861	40.7	551 1	LEM2_RABIT
16	860	40.6	611 1	LEM2_CANFA
17	858.5	40.6	549 1	LEM2_RAT
18	857	40.5	612 1	LEM2_MOUSE
19	849.5	40.1	485 1	LEM2_BOVIN
20	814.5	38.5	484 1	LEM2_PIG
21	212.5	10.0	1019 1	LFC_TACTR
22	199.5	9.4	1231 1	CEAH_HUMAN
23	195	9.2	958 1	HIG_DROME
24	189.5	9.0	1019 1	LFC_CARRO
25	172	8.1	2039 1	CRI_HUMAN
26	171	8.1	564 1	PGCA_CANFA
27	168	7.9	2132 1	PGCA_MOUSE
28	167	7.9	321 1	FCE2_HUMAN
29	167	7.9	1234 1	CRAH_MOUSE
30	166.5	7.9	558 1	CABP_RAT
31	166	7.8	390 1	DAFI_MOUSE
32	166	7.8	1456 1	MANR_HUMAN
33	166	7.8	2364 1	PGCA_BOVIN

34	165	7.8	311 1	LECI_HUMAN	P07307 homo sapien
35	165	7.8	548 1	KUCR_MOUSE	P70194 mus musculus
36	163	7.7	2124 1	PGCA_RAT	P07897 rattus norv
37	162.5	7.7	345 1	APDH_BOVIN	P17690 bos taurus
38	162	7.7	304 1	MGML_MOUSE	P49300 mus musculus
39	160	7.6	2415 1	PGCA_HUMAN	P16112 homo sapien
40	157	7.4	331 1	FCE2_MOUSE	P20693 mus musculus
41	157	7.4	469 1	CABP_MOUSE	P08607 mus musculus
42	157	7.4	610 1	CABP_BOVIN	Q28065 bos taurus
43	156.5	7.4	207 1	LECH_CHICK	P03707 gallus gall
44	156.5	7.4	1025 1	CR2_MOUSE	P19070 mus musculus
45	156	7.4	258 1	CABP_RAT	Q63515 rattus norv

ALIGNMENTS

RESULT	ID	LEM1_HUMAN	STANDARD:	PRT:	372 AA.
AC	P14151	P15023			
DT	01-JAN-1990	(rel. 13, Created)			
DT	01-FEB-1991	(rel. 17, Last sequence update)			
DT	30-MAY-2000	(rel. 39, Last annotation update)			
DE	L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (T01) (GP90-MEL)				
DE	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L).				
CN	SELL OR LYAM1 OR LNHK.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=89315837; PubMed=2664786;				
RA	Siegelman M.H., Weissman I.L.;				
RT	"Human homologue of mouse lymph node homing receptor: evolutionary conservation at tandem cell interaction domains.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 86:5562-5566(1989).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISUE=TONSIL;				
RX	MEDLINE=89310350; PubMed=2473156;				
RA	Tedder T.F., Isaacs C.M., Ernst T.J., Demetri G.D., Adler D.A.,				
RA	Disteche C.M.;				
RT	"Isolation and chromosomal localization of cDNAs encoding a novel human lymphocyte cell surface molecule, LAM-1. Homology with the mouse lymphocyte homing receptor and other human adhesion proteins.";				
RL	J. Exp. Med. 170:123-133(1989).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90044046; PubMed=2509939;				
RA	Camerini D., James S.P., Stamenkovic I., Seed B.;				
RT	"Leu-8/T01 is the human equivalent of the Mel-14 lymph node homing receptor.";				
RL	Nature 342:78-82(1989).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=89308881; PubMed=2663882;				
RA	Bowen B.R., Nguyen T., Lasky L.A.;				
RT	"Characterization of a human homologue of the murine peripheral lymph node homing receptor.";				
RL	J. Cell Biol. 109:421-427(1989).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90243637; PubMed=1692315;				
RA	Ord D.C., Ernst T.J., Zhou L.J., Rambaldi A., Spectini O.,				
RA	Griffin J., Tedder T.F.;				
RT	"Structure of the gene encoding the human leukocyte adhesion molecule-1 (T01, Leu-8) of lymphocytes and neutrophils.";				
RL	J. Biol. Chem. 265:7760-7767(1990).				
CC	-1- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATES THE ADHERENCE OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL				
CC	VENULES IN PERIPHERAL LYMPH NODES.				

Query Match	Best Local Similarity	98.8%;	Score 2090;	DB 1;	Length 372;
Matches 368;	Conservative	1;	Mismatches 3;	Indels 0;	Gaps 0;
FT CARBOHYD	232	232	N-LINKED (GLCNAC. . .)	(POTENTIAL).	
FT CARBOHYD	246	246	N-LINKED (GLCNAC. . .)	(POTENTIAL).	
FT CARBOHYD	271	271	N-LINKED (GLCNAC. . .)	(POTENTIAL).	
FT CARBOHYD	311	311	N-LINKED (GLCNAC. . .)	(POTENTIAL).	
FT CONFLICT	37	37	D -> Y (IN REF. 4).		
FT CONFLICT	178	178	Y -> H (IN REF. 4).		
FT CONFLICT	193	193	F -> L (IN REF. 1 AND 4).		
FT CONFLICT	213	213	P -> S (IN REF. 3).		
FT CONFLICT	214	214	L -> F (IN REF. 4).		
FT CONFLICT	218	220	SFS -> NFN (IN REF. 2).		
FT CONFLICT	242	242	G -> E (IN REF. 2).		
SQ SEQUENCE	372 AA;	42187 MW;	6EA9918E0CA2D3643	CRC64;	
Query Match	98.8%;	Score 2090;	DB 1;	Length 372;	
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QY 1 MIPPMKCSSTORDLNINIFKLMGWTMLCCDFLAHGTQWYTHYSEKPMNQRARPCRDN 60					
DB 1 MIPPMKCSSTORDLNINIFKLMGWTMLCCDFLAHGTQWYTHYSEKPMNQRARPCRDN 60					
QY 61 YVDLVAIQKADIEYLEKTLPPSRSYWIGIKIGTIGITWTGTSKSLTEEAENMGDGEPN 120					
DB 61 YVDLVAIQKADIEYLEKTLPPSRSYWIGIKIGTIGITWTGTSKSLTEEAENMGDGEPN 120					
QY 121 NKKNNKDCVEIYIKRNNKAGKNDADCAKRLKAALCYTASCPWAGSCGHGCEVEIYNHTC 180					
DB 121 NKKNNKDCVEIYIKRNNKAGKNDADCAKRLKAALCYTASCPWAGSCGHGCEVEIYNHTC 180					
QY 181 NCDVGYGPOCLVIOCEPLLEAPLELGTMDCTHPFGNFSFSOCAFSCSEGNLTGIEET 240					
DB 181 NCDVGYGPOCLVIOCEPLLEAPLELGTMDCTHPFGNFSFSOCAFSCSEGNLTGIEET 240					
QY 241 CGPFGNMSSPEPTCOYIOCEPLSAPDLGIMNCSHPLASFSTSCACFICSEGTIELGKKK 300					
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QY 301 TICESGSGIMSNPSPICOLDKFSFMIRKGDVNPFIYVAWVAVAFSLATITWLARIRK 360					
DB 301 TICESGSGIMSNPSPICOLDKFSFMIRKGDVNPFIYVAWVAVAFSLATITWLARIRK 360					
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DB 361 GKSKSRSMNDPY 372					
RESULT 2					
LEML_PANTR	STANDARD;	PRT;	372 AA.		
AC 095237;					
DT 01-NOV-1997 (Rel. 35, Created)					
DT 01-NOV-1997 (Rel. 35, Last sequence update)					
DT 01-NOV-1997 (Rel. 35, Last annotation update)					
DE L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LPCAM1) (CD62L).					
DE GN					
OS Pan troglodytes (Chimpanzee).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.					
RN [1]					
RP SEQUENCE FROM N.A.					
RA Budman J.I., Fu H., Johnson C.E., Thakur A.B., Berg E.L.,					
RA Tsurushita N.;					
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.					
CC -1- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIANE THE ADHERENCE OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL					
CC VENUES IN PERIPHERAL LYMPH NODES.					
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.					
CC -1- SIMILARITY: TO OTHER SELECTINS/LBECAMS.					
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.					
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.					

```

CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U73728; AAB18248.1; -.
DR HSSP: P14151; IKJB.
DR INTERPRO: IPR000436; -.
DR INTERPRO: IPR000561; -.
DR INTERPRO: IPR001304; -.
DR INTERPRO: IPR002396; -.
DR PFAM: PF00008; EGF_1.
DR PFAM: PF00059; Lectin_C; 1.
DR PFAM: PF00084; sush1; 2.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00615; C-TYPE-LECTIN_1; 1.
DR PROSITE: PS50041; C-TYPE-LECTIN_2; 1.
DR Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sush1; Repeat.
FT SIGNAL 1 28
FT PROPEP 29 38
FT CHAIN 39 372
FT DOMAIN 39 332
FT TRANSMEM 333 355
FT DOMAIN 356 372
FT DOMAIN 55 155
FT DOMAIN 156 192
FT DOMAIN 196 317
FT REPEAT 196 255
FT REPEAT 258 317
FT DISULFID 57 155
FT DISULFID 128 147
FT DISULFID 160 171
FT DISULFID 165 180
FT DISULFID 182 191
FT DISULFID 197 241
FT DISULFID 227 254
FT DISULFID 259 303
FT DISULFID 289 316
FT CARBOHYD 60 60
FT CARBOHYD 104 104
FT CARBOHYD 177 177
FT CARBOHYD 216 216
FT CARBOHYD 232 232
FT CARBOHYD 246 246
FT CARBOHYD 271 271
SO SEQUENCE 372 AA; 42188 MW; 6EA991802AD3643 CRC64;

Query Match 98.5% Score 2085; DB 1; Length 372;
Best Local Similarity 98.7% Pred. No. 3.9e-158;
Matches 367; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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DB 181 NCDVGYGQCFVIOCEPLAPLGTMDCTHPHLCNFSFSOCARSCSGVLTG1 EFTT 240
QY 241 GCPFNWMSPEPTCOVIOCEPLASPDIGIMNCSHPLASFSFASCTFCSEGTILGKK 300
DB 241 GCPFNWMSPEPTCOVIOCEPLASPDIGIMNCSHPLASFSFASCTFCSEGTILGKK 300
QY 301 TFCSSGIMSNPSPIQOKKDKSFSMIKEGDYPLPLPAVAVWYAFSGLAFTIWLARRLKK 360
DB 301 TFCSSGIMSNPSPIQOKKDKSFSMIKEGDYPLPLPAVAVWYAFSGLAFTIWLARRLKK 360
QY 361 GKSKSRSMNDPY 372
DB 361 GKSKSRSMNDPY 372

RESULT 3
LEML_PONPY STANDARD; PRT; 372 AA.
ID LEML_PONPY
AC Q95235;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L).
DE SEL.
GN Pongo pygmaeus (Orangutan).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pongo.
RN [1]
RP SEQUENCE FROM N.A.
RA Budman J.I., Fu H., Johnson C.E., Thakur A.B., Berg E.L.,
RA Tsurushita N.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATES THE ADHERENCE OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL VENULES IN PERIPHERAL LYMPH NODES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMs.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U73729; AAB18247.1; -.
DR HSSP: P14151; IKJB.
DR INTERPRO: IPR000436; -.
DR INTERPRO: IPR000561; -.
DR INTERPRO: IPR001304; -.
DR INTERPRO: IPR002396; -.
DR PFAM: PF00008; EGF_1.
DR PFAM: PF00059; Lectin_C; 1.
DR PFAM: PF00084; sush1; 2.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00615; C-TYPE-LECTIN_1; 1.
DR PROSITE: PS50041; C-TYPE-LECTIN_2; 1.
DR Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sush1; Repeat.
FT SIGNAL 1 28
FT PROPEP 29 38
FT CHAIN 39 372
FT DOMAIN 39 332
FT TRANSMEM 333 355

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FT DOMAIN 356 372 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 35 155 C-TYPE LECTIN (SHORT FORM).
FT DOMAIN 156 192 EGF-LIKE.
FT DOMAIN 196 317 2 X SUSHI (SCR) REPEATS.
FT REPEAT 196 255 SUSHI 1.
FT REPEAT 258 317 SUSHI 2.
FT DISULFID 57 155 BY SIMILARITY.
FT DISULFID 128 147 BY SIMILARITY.
FT DISULFID 160 171 BY SIMILARITY.
FT DISULFID 165 180 BY SIMILARITY.
FT DISULFID 182 191 BY SIMILARITY.
FT DISULFID 197 241 BY SIMILARITY.
FT DISULFID 227 254 BY SIMILARITY.
FT DISULFID 259 303 BY SIMILARITY.
FT DISULFID 289 316 BY SIMILARITY.
FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 372 AA: 42118 MW: 6517DD22213PF15E CRC64:

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Query Match 97.4% Score 2062; DB 1; Length 372;
Best Local Similarity 97.6% Pred. No. 2.6e-156;
Matches 363; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MIFPKCSTOGLDNLNFKLMGTMKCDPLAHGTCMTYHSKPKMNMQRARFCNDN 60
DB 1 MIFPKCSTOGLDNLNFKLMGTMKCDPLAHGTCMTYHSKPKMNMQRARFCNDN 60
QY 61 YTDVAIONKAEIEYLEKTLPEFSRSYWGIRKIGIWTWGTNKSLEAEANMGDGP 120
DB 61 YTDVAIONKAEIEYLEKTLPEFSRSYWGIRKIGIWTWGTNKSLEAEANMGDGP 120
QY 121 NKKNKDEVEIYIKRNKAGKNDACKKLAALCYTASCPWSCSGHGEVEIINNHTC 180
DB 121 NKKNKDEVEIYIKRNKAGKNDACKKLAALCYTASCPWSCSGHGEVEIINNHTC 180
QY 181 NCDVGYGPOGLVIOCEPLAPELGTMDCTHPGNSFSSOCAPFSGEGNLTGIEET 240
DB 181 NCDVGYGPOGLVIOCEPLAPELGTMDCTHPGNSFSSOCAPFSGEGNLTGIEET 240
QY 241 CGPFGNMSSPEPTCOVIOCEPLAPDLGIMNCSHPLASFSTACTFICSGETELIGKK 300
DB 241 CGPFGNMSSPEPTCOVIOCEPLAPDLGIMNCSHPLASFSTACTFICSGETELIGKK 300
QY 301 TICSSSGIWSNPSPICKIDKSFMSIKEGDVPNFYVAWVTFEAGIATIMLARLKK 360
DB 301 TICSSSGIWSNPSPICKIDKSFMSIKEGDVPNFYVAWVTFEAGIATIMLARLKK 360
QY 361 GKSKRSKNDPY 372
DB 361 GKSKRSKNDPY 372

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RESULT 4
LEMI_MACMU STANDARD: PRT: 372 AA.
AC 095198:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE I-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUCOCYTE ADHESION MOLECULE-1) (LAW-1) (LEUCOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L).
DE GN SEILL.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

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OC Cercopithecoidea; Macaca.
RN [1]
RP Sequence from N.A.
RA Budman J., Fu H., Johnson C.E., Thakur A.B., Berg E.L.,
RA Tsurushita N.
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC - FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATES THE ADHESION
CC OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL
CC VENULES IN PERIPHERAL LYMPH NODES.
CC - SUBCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN.
CC - SIMILARITY: TO OTHER SELECTINS/LECAMs.
CC - SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC - SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC - SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U73730; AB18246.1; -
DR HSSP: P14151; IKB.
DR INTERPRO: IPR000436; -
DR INTERPRO: IPR000561; -
DR INTERPRO: IPR001304; -
DR INTERPRO: IPR002396; -
DR PRAM: PF00008; EGF_1.
DR PFAM: PF00059; LECTIN_C_1.
DR PFAM: PF00084; SUSHI_2.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE: PS00615; C-TYPE_LECTIN_2; 1.
DR PROSITE: PS00615; C-TYPE_LECTIN_2; 1.
KW Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sush; Repeat.
FT SIGNAL 1 28
FT PROPEP 29 38
FT CHAIN 39 372
FT DOMAIN 39 332 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 333 355 POTENTIAL.
FT DOMAIN 356 372 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 55 155 C-TYPE LECTIN (SHORT FORM).
FT DOMAIN 156 192 EGF-LIKE.
FT DOMAIN 196 317 2 X SUSHI (SCR) REPEATS.
FT REPEAT 196 255 SUSHI 1.
FT REPEAT 258 317 SUSHI 2.
FT DISULFID 57 155 BY SIMILARITY.
FT DISULFID 128 147 BY SIMILARITY.
FT DISULFID 160 171 BY SIMILARITY.
FT DISULFID 165 180 BY SIMILARITY.
FT DISULFID 182 191 BY SIMILARITY.
FT DISULFID 197 241 BY SIMILARITY.
FT DISULFID 227 254 BY SIMILARITY.
FT DISULFID 259 303 BY SIMILARITY.
FT DISULFID 289 316 BY SIMILARITY.
FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 372 AA: 42109 MW: 088D/DD5AC549D6D CRC64:

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Query Match 94.3% Score 1996; DB 1; Length 372;
Best Local Similarity 93.8% Pred. No. 4.4e-151;
Matches 349; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

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QY 1 MIEPRKCGSTORDLWNIEFLMGWMLCDFLAHNGTCWTYHSEKPMNMQRARFCRDN 60
DB 1 MIEPRKCGSTORDLWNIEFLMGWMLCDFLAHNGTCWTYHSEKPMNMQRARFCRDN 60
QY 61 YTDVAIONKAEIYLEKTLPPSRSYWYIGIRKIGITWVGTNKSLTDEAENMGDGEFN 120
DB 61 YTDVAIONKAEIYLEKTLPPSRSYWYIGIRKIGITWVGTNKSLTDEAENMGDGEFN 120
QY 121 NKKNKEDCEVEIYIKRKNKDGKNNDDACHLKAALCYTASCQPMSCSGHCEVEIINNHTC 180
DB 121 NKKNKEDCEVEIYIKRKNKDGKNNDDACHLKAALCYTASCQPMSCSGHCEVEIINNHTC 180
QY 181 NCDVGYGPOCQVIOCEPLLEPPLGTMCTHPFGNFSFSOCAPSCSEGTNLGIEETT 240
DB 181 NCDVGYGPOCQVIOCEPLLEPPLGTMCTHPFGNFSFSOCAPSCSEGTNLGIEETT 240
QY 241 CGPFGNWSSEPTTCOVIOCEPLSAPDLGIMNCSHPLASFSFSACFTFCSEGTNLGK 300
DB 241 CGPFGNWSSEPTTCOVIOCEPLSAPDLGIMNCSHPLASFSFSACFTFCSEGTNLGK 300
QY 301 TICSSGIMSNPSPIQOKLDRSFSMIKBDYVPLFIPVAVMTAFSGLAFTIWLARLKK 360
DB 301 TICSSGIMSNPSPIQOKLDRSFSMIKBDYVPLFIPVAVMTAFSGLAFTIWLARLKK 360
QY 361 GKSKRSMDPY 372
DB 361 GKSKRSMDPY 372

RESULT 5

LEML_PAPHA STANDARD: PRT: 372 AA.

AC 028768:

DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).
GN SELL.

OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.

RE SEQUENCE FROM N.A.

RA MEDLINE-97128794; PubMed-8973334;

RT "PCR cloning of the cDNA encoding baboon L-selectin.";

RL Gene 181:219-220(1996).

CC -I- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATES THE ADHERENCE

CC OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL

CC VENULES IN PERIPHERAL LYMPH NODES.

CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -I- SIMILARITY: TO OTHER SELECTINS/LECAMs.

CC -I- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

CC -I- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

CC -I- SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.

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CC or send an email to license@isb-sib.ch).

CC EMBL: U52074; AAB40903.1; -

DR HSSP: P14151; ICRB.

DR INTERPRO: IPR000436; -

DR INTERPRO: IPR000561; -

DR INTERPRO: IPR001304; -

DR INTERPRO: IPR002396; -

DR PFAM: PF00008; EGF_1.
DR PFAM: PF00059; lectin_c. 1.
DR PFAM: PF00084; sushi. 2.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE: PS00041; C-TYPE LECTIN_2; 1.
DR Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sushi; Repeat.
FT SIGNAL 1 28
FT PROPEP 29 38
FT CHAIN 39 372
FT DOMAIN 39 332
FT TRANSMEM 333 355
FT DOMAIN 356 372
FT DOMAIN 55 155
FT DOMAIN 156 192
FT DOMAIN 196 317
FT REPEAT 196 255
FT REPEAT 258 317
FT DISULFID 57 155
FT DISULFID 128 147
FT DISULFID 160 171
FT DISULFID 165 180
FT DISULFID 182 191
FT DISULFID 197 241
FT DISULFID 227 254
FT REPEAT 259 303
FT DISULFID 289 316
FT CARBOHYD 60 60
FT CARBOHYD 104 104
FT CARBOHYD 177 177
FT CARBOHYD 226 226
FT CARBOHYD 232 232
FT CARBOHYD 246 246
FT CARBOHYD 271 271
SO SEQUENCE 372 AA; 42091 MW; 64E7BDD5AC549D69 CRC64;

Query Match 94.1%; Score 1992; DB 1; Length 372;

Best Local Similarity 93.5%; Pred. No. 9,1e-151;

Matches 348; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 1 MIEPRKCGSTORDLWNIEFLMGWMLCDFLAHNGTCWTYHSEKPMNMQRARFCRDN 60
DB 1 MIEPRKCGSTORDLWNIEFLMGWMLCDFLAHNGTCWTYHSEKPMNMQRARFCRDN 60
QY 61 YTDVAIONKAEIYLEKTLPPSRSYWYIGIRKIGITWVGTNKSLTDEAENMGDGEFN 120
DB 61 YTDVAIONKAEIYLEKTLPPSRSYWYIGIRKIGITWVGTNKSLTDEAENMGDGEFN 120
QY 121 NKKNKEDCEVEIYIKRKNKDGKNNDDACHLKAALCYTASCQPMSCSGHCEVEIINNHTC 180
DB 121 NKKNKEDCEVEIYIKRKNKDGKNNDDACHLKAALCYTASCQPMSCSGHCEVEIINNHTC 180
QY 181 NCDVGYGPOCQVIOCEPLLEPPLGTMCTHPFGNFSFSOCAPSCSEGTNLGIEETT 240
DB 181 NCDVGYGPOCQVIOCEPLLEPPLGTMCTHPFGNFSFSOCAPSCSEGTNLGIEETT 240
QY 241 CGPFGNWSSEPTTCOVIOCEPLSAPDLGIMNCSHPLASFSFSACFTFCSEGTNLGK 300
DB 241 CGPFGNWSSEPTTCOVIOCEPLSAPDLGIMNCSHPLASFSFSACFTFCSEGTNLGK 300
QY 301 TICSSGIMSNPSPIQOKLDRSFSMIKBDYVPLFIPVAVMTAFSGLAFTIWLARLKK 360
DB 301 TICSSGIMSNPSPIQOKLDRSFSMIKBDYVPLFIPVAVMTAFSGLAFTIWLARLKK 360
QY 361 GKSKRSMDPY 372
DB 361 GKSKRSMDPY 372


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RESULT 6
LEML_BOVIN
ID LEML_BOVIN STANDARD: PRT: 370 AA.
AC P98131;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L).
GN SELL.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=92164727; PubMed=1371468;
RA Walcheck B., White M., Kurk S., Kishimoto T.K., Jutila M.A.;
RT "Characterization of the bovine peripheral lymph node homing receptor: a lectin cell adhesion molecule (LECAM).";
RL Eur. J. Immunol. 22:469-476(1992).
RN SEQUENCE FROM N.A.
RX MEDLINE=9405053; PubMed=7694420;
RA Bosworth B.T., Dombenke D., Shuster D.E., Harp J.A.;
RT "Bovine L-selectin: a peripheral lymphocyte homing receptor.";
RL Vet. Immunol. Immunopathol. 37:201-215(1993).
CC -1- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATES THE ADHERENCE OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL VENULES IN PERIPHERAL LYMPH NODES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
CC -----
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CC -----
DR EMBL: X62882; CAA44676.1; -
DR HSSP: P14151; IKTJ
DR INTERPRO: IPR000436; -
DR INTERPRO: IPR000561; -
DR INTERPRO: IPR001304; -
DR INTERPRO: IPR002396; -
DR PFAM: PF00008; EGF_1.
DR PFAM: PF00059; lectin.C.1.
DR PFAM: PF00084; sushi_2.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE: PS50041; C-TYPE LECTIN_2; 1.
KW Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sushi; Repeat.
FT SIGNAL 1 28
FT PROPEP 29 38
FT CHAIN 39 370
FT DOMAIN 39 333
FT TRANSMEM 334 354
FT DOMAIN 355 370
FT DOMAIN 55 155
FT DOMAIN 156 192
FT DOMAIN 196 317
FT REPEAT 196 255
FT REPEAT 258 317
FT DISULFID 57 155
BY SIMILARITY.

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FT DISULFID 128 147 BY SIMILARITY.
FT DISULFID 160 171 BY SIMILARITY.
FT DISULFID 165 180 BY SIMILARITY.
FT DISULFID 182 191 BY SIMILARITY.
FT DISULFID 197 241 BY SIMILARITY.
FT DISULFID 227 254 BY SIMILARITY.
FT DISULFID 259 303 BY SIMILARITY.
FT DISULFID 289 316 BY SIMILARITY.
FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 370 AA; 41971 MW; 92168P8116A89228 CRC64;

Query Match
Best Local Similarity 79.5%; Score 1682; DB 1; Length 370;
Matches 282; Conservative 42; Mismatches 40; Indels 2; Gaps 1;

QY 1 MIFPKCSTORDIMNIRKMGWIMLCDDPLAHNGTCWTYHSEKPMNQARARFCRON 60
D 1 MCEPKCQNAQRGLMNVFKLWIMLCDDFAHNGTCWTYHSEKPMNEKARARFCREN 60
D 1 YTDLVAIONKAEIYELKTLPEFSRSYYWIGIRKIGITWYWGINKSLTEBAEWMSGCEPN 120
D 61 YTDLVAIONKAEIYELKTLPEFSRSYYWIGIRKIGITWYWGINKSLTEBAEWMSGCEPN 120
QY 121 NKKRKECCVEIYIRKNDACKNDACKIKALKCYTASQCPMSGSGHCEYIINHTC 180
D 121 NKRKECCVEIYIRKNDACKNDACKIKALKCYTASQCPMSGSGHCEYIINHTC 180
QY 181 NCDVGYGPOCULVTOCEPLEAPELGTMOCTHPGMSFSSOCAPSCSGTUNLGEFT 240
D 181 NCDVGYGPOCULVTOCEPLEAPELGTMOCTHPGMSFSSOCAPSCSGTUNLGEFT 240
QY 241 CGPGNMSSEPPICQYVYCEPLAPDLGIMNCSHPLASPSFTSACTYFTESETELGKK 300
D 241 CAPGNMSSEPPICQYVYCEPLAPDLGIMNCSHPLASPSFTSACTYFTESETELGKK 300
QY 301 TIGSSGIMNPNPICOIKDKDSFMKEGDYNPFLPVAVMYTAASGLAFITWLARKK 360
D 301 TIGGLSNNSSPSPROCKINRTISTINESDYNPFLPVAVMYTAASGLAFITWLARKK 360
QY 361 GKRSKR 366
D 361 GKRSKR 364
D 360 -RKSRR 364

RESULT 7
LEML_RAT
ID LEML_RAT STANDARD: PRT: 372 AA.
AC P30836;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LY-22) (LYMPHOCYTE SURFACE MEL-14 ANTIGEN) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L).
GN SELL OR LYMR OR LY-22.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=92329548; PubMed=1378303;
RA Watanabe T., Song Y., Hirayama Y., Tametani T., Kuida K., Miyasaka M.;
RT "Sequence and expression of a rat cDNA for LECAM-1.";
RL Biochim. Biophys. Acta 1131:321-324(1992).

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CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X14772; CA32880.1; -
DR EMBL: M36005; AAA39722.1; -
DR EMBL: M36058; AAA39723.1; -
DR EMBL: M25324; -; NOT_ANNOTATED_CDS.
DR EMBL: M64549; AAA75651.1; -
DR EMBL: M64440; AAA75651.1; JOINED.
DR EMBL: M64545; AAA75651.1; JOINED.
DR EMBL: M64548; AAA75651.1; JOINED.
DR PIR: A32375; A32375.
DR HSSP: P14151; IKUH.
DR MGD: MGI:96279; SELL.
DR INTERPRO: IPR000436; -.
DR INTERPRO: IPR000561; -.
DR INTERPRO: IPR001304; -.
DR INTERPRO: IPR002386; -.
DR PFAM: PF00008; EGF_1.
DR PFAM: PF00059; Lectin_c; 1.
DR PFAM: PF00084; sushi; 2.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE: PS00186; EGF_2; 1.
DR PROSITE: PS50041; C-TYPE LECTIN_2; 1.
DR Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sushi; Repeat.
KM
FT SIGNAL 1 28
FT PROPEP 29 38
FT CHAIN 39 372
FT DOMAIN 39 332
FT TRANSMEM 333 355
FT DOMAIN 356 372
FT DOMAIN 55 155
FT DOMAIN 156 192
FT DOMAIN 196 317
FT REPEAT 196 255
FT REPEAT 258 317
FT DISULFID 57 155
FT DISULFID 128 147
FT DISULFID 160 171
FT DISULFID 165 180
FT DISULFID 182 191
FT DISULFID 197 241
FT DISULFID 227 254
FT DISULFID 259 303
FT DISULFID 289 316
FT CARBOHYD 60 104
FT CARBOHYD 104 177
FT CARBOHYD 177 216
FT CARBOHYD 216 226
FT CARBOHYD 226 246
FT CARBOHYD 246 278
FT CARBOHYD 288 288
FT CARBOHYD 308 308
FT CARBOHYD 320 320
FT CONFLICT 32 32
FT SOURCE 372 AA; 42288 MM; 4433EDPEACB2B78 CRC64;

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Query Match 78.0%; Score 1651; DB 1; Length 372;
 Best Local Similarity 76.1%; Pred. No. 9, 1e-124;
 Matches 283; Conservative 32; Mismatches 57; Indels 0; Gaps 0;

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QY 1 MTFPMKCGSTORDLWNIKFKMGWIMLCDFLAHGTGYCWTYHSEKPMNMORARFCRDN 60
Db 1 MTFPMKCGSTGYWGSRNITKLWMTLLCDEFILHGHGTHCMYHSEKPMNMENARKFCRDN 60
QY 61 YNDLVAIQKAEILEYLEKTLFPSRSYWNIGTRIGGTTWGTNKSLSLEENMGDDEPN 120
Db 61 YNDLVAIQKREILEYLENTLPKSPYWNIGTRIGGTTWGTNKTITKEAENMGAGEPN 120
QY 121 NKKNEDEVEIYIKRNKDKAGKNDACRKLKAALCYTASCPMKSQSGHCEVEIINNHTC 180
Db 121 NKKSEDEVEIYIKRERDSGKWNDDACHKRAALCYTASCPGSGNGRCEVEIINNHTC 180
QY 181 NDDVGYVPGQOLVYQCEPLAPELGTMDCTHPGNSFSQCAFSCSEGTNLITGIEET 240
Db 181 ICDADYVPGQCYVQCEPLAPELGTMDCTHPGNSFSQCAFSCSEGTNLITGIEET 240
QY 241 CGPFGNMSPPETCOVICPELSPADGIMNCSPHLASFSTACTCTICEGELLGKK 300
Db 241 CGASGNMSPPETCOVQCEPLAPELGTMDCTHPGNSFSQCAFSCSEGTNLITGIEET 300
QY 301 TICSSGIWNSPPIQKLDKFSMIKEGDYNPFIPIVAVMTAFSGIAFIIMLARRLKK 360
Db 301 TQCGASGNMSPPETCOVQCEPLAPELGTMDCTHPGNSFSQCAFSCSEGTNLITGIEET 360
QY 361 GKSKRSMNDPY 372
Db 361 GKSKRSMNDPY 372

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RESULT 9
LEM3_SHEEP STANDARD; PRT; 769 AA.
ID LEM3_SHEEP
AC P98109;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM
DE (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
GN SELP.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RA Burns S.A., Neufeld E.J., Donady J.J.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
CC TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
CC INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
CC LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMs.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
CC -1- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L34270; AAB59261.1; -
DR HSSP: P16109; IFSB.
DR INTERPRO: IPR000436; -.
DR INTERPRO: IPR000561; -.
DR INTERPRO: IPR001304; -.
DR INTERPRO: IPR002386; -.
DR PFAM: PF00008; EGF_1.

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Db	65	TDVLAIOKKNELAVLNLNETIIPYNSYTWGIRKIDNKMTWTCKTTLTLEENNAWADNEPNN	12
QY	122	KNNEDEVEIYIKRKNKQAKWNNDDACHLKAALCYTASQCPMSGSGHGEVEIINNHTCN	181
Db	125	KKNNDQCEVEIYIKPSAPGKKNWDEPCGRKKRALCYRASQCPMSKQCECIETITGNVTC	184
QY	182	CDVGYGGQCCOLVYQCEPLEPELGTMDCTHPFENFSSQCAFGSGEGTNLGIETTC	244
Db	185	CYPGYGEGCEYVRECGEFDLPQVHNHMCSPHLGNFSPKSCSPHCAEGYALNPRLECC	244
QY	242	GPFGKSSPEPTCOVIOCEPLASDPLGIMNSHPILASFSPISACTPFCISGTELGKKT	301
Db	245	LASGTWTSPPQCAVAVCCPALKSEFGSGMSCFHAKAFQHOSSCSFCEGFTLVGEVY	304
QY	302	ICESSGIMSNPSPIQOKL 319	
Db	305	HTALGVTWTAFTPYCKAI 322	
RESULT	10		
LEM3	HUMAN	STANDARD;	PRT; 830 AA.
ID	LEM3_HUMAN	STANDARD;	PRT; 830 AA.
AC	PI6109;		
DT	01-APR-1990 (Rel. 14, Created)		
DT	01-AUG-1990 (Rel. 15, Last sequence update)		
DT	01-OCT-2000 (Rel. 40, Last annotation update)		
DE	P-SELECTIN PRECURSOR (GRAULE MEMBRANE PROTEIN 140) (GMP-140) (PADGE		
DE	(CG62P) (LEUCOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3),		
GN	SELP OR GMPR		
OS	Homo sapiens (Human).		
OC	Eumetazoa; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
NP	11		
RP	SEQUENCE FROM N.A.		
RP	MEDLINE=89168432; PubMed=2466574;		
RX	Medline=93266599; PubMed=7684381;		
RA	Fujimoto T., Stroud E., Whalley R.E., Prescott S.M., Muszbek L.,		
RA	Laposata M., McEver R.P.;		
RT	"P-selectin is acylated with palmitic acid and stearic acid at		
RT	cysteine 766 through a thioester linkage.";		
RL	J. Biol. Chem. 268:11394-11400(1993).		
RL	[3]		
RN	STRUCTURE BY NMR OF 160-199.		
RP	MEDLINE=97057176; PubMed=9901515;		
RX	Medline=94093388; PubMed=7505680;		
RA	Freedman S.J., Sanford D.G., Bachovich W.W., Furie B.C., Bajaja J.D.,		
RA	Furie B.;		
RT	"Structure and function of the epidermal growth factor domain of P-		
RT	selectin.";		
RL	Biochemistry 35:13733-13744(1996).		
RN	[4]		
RP	3D-STRUCTURE MODELING OF 42-161.		
RX	Medline=94093388; PubMed=7505680;		
RA	Bajorath J., Stenkamp R., Aurilio A.;		
RT	"Knowledge-based model building of proteins: concepts and examples.";		
RT			

RP. VARIANTS ASN-331; ASP-603; VAL-640 AND PRO-756.
RX. MEDLINE=98334547; Pubmed=9668170;
RA. Herrmann S.M., Ricard S., Nicaud V., Mallet C., Evans A.,
RA. Rudavets J.B., Arveiler D., Luc G., Cambien F.,
RT. The P-selectin gene is highly polymorphic: reduced frequency of the
RT. pro705 allele carriers in patients with myocardial infarction.,"
RL. Hum. Mol. Genet. 7:11277-1284(1998).
-I- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
CC. TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
CC. INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH

[illegible]

Query Match	Best Local Similarity	Matches 157; Conservative 47; Mismatches 106; Indels 0; Gaps 0.
QY 8 OSTQDMDLNNIRKLMGWTMLCCDFLAHHGTYCMTYHSEKPNMOWRARFCNDYTDVLAI 67	42.8%; Score 905; DB 1; Length 830;	
Db 11 OFQGVVWFISQLLCSFALISLITLNOKEVAAMTYSTKAYSMNISRYCCONRTDVLAI 70	50.6%; Pred. No. 2.6e-64;	
QY 68 ONKEIEYLEKTPFSRSYWIIGIRKIGITWYWTNSLLEEDLNNGDEPPNNKKKED 127		
Db 71 ONKNRDIPLKLVVYSSYWIIOIRKNNKTYWVTGKALTLNEENADNEPPNNKRNED 130		
QY 128 CVELYIKRNDACKNNDACHKIKALCYTASQFWSGSHGCEVETIINNHTCNCVGY 187		
Db 131 CVELYIKSPSAPKRWDEHLKKKHALCYTASQFWSGSHGCEVETIINNHTCNCVGY 190		
QY 188 GPQCOLVIOCEPLEAFELGTMDCTHPEFGNFSFSSQCAFQSGEGINLTGLETTGCGFNM 247		
Db 191 GPCECVVREGCELELPHQHLAMCSHPLCNFSNOCSTHCTGYVNGPSEKCLASGIW 250		
QY 248 SSEPTQVYIQCEPPLSAPDLGIMNCSHPLASFSYTSACTGTCSEGTLLGKKKTKCSG 307		
Db 251 TNNPQCLAAOCPLKTPERGNNICLHSAKFKFQHQSSCSFGSGEFGALVCPMVOGTAC 310		

QY 308 IWSNPSPICQ 317
: : : : :
Db 311 VMTAPAPVCK 320

RESULT 11
LEMS_MOUSE STANDARD; PRT; 768 AA.

AC 001102;
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 40, Last annotation update)
DE P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
DE (CD62P) (LEUCOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
DE SELP OR GRMP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE-92340571; PubMed-1378846;
RA Weller A., Isenmann S., Vestweber D.;
RT "Cloning of the mouse endothelial selectins. Expression of both E-
RT and P-selectin is inducible by tumor necrosis factor alpha.";
RL J. Biol. Chem. 267:15176-15183(1992).
RN 121
RP SEQUENCE FROM N.A.
RX MEDLINE-92345617; PubMed-1379089;
RA Sanders W.E. Jr., Willson R.W., Ballantyne C.M., Beaudet A.L.;
RT "Molecular cloning and analysis of in vivo expression of murine P-
RT selectin.";
RL Blood 80:795-800(1992).
CC -1- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
CC TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
CC INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
CC LEUKOCYTES. THE LIGAND RECOGNIZED IS STALYL-LEWIS X.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS
CC AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
CC ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
CC THE CELL SURFACE.
CC -1- INDUCTION: BY TUMOR NECROSIS FACTOR ALPHA.
CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMs.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS. MOUSE P-LECTIN LACKS
CC THE HUMAN SUSHI-2 EQUIVALENT.
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CC -----
DR EMBL: M87861; AAA4008.1; -;
DR EMBL: M72332; AAA3712.1; -;
DR PIR: A42755; A42755.
DR HSSP: P16109; 1FSB.
DR MGD: MGI:98280; SELP.
DR INTERPRO: IPR000436; -;
DR INTERPRO: IPR000561; -;
DR INTERPRO: IPR001304; -;
DR INTERPRO: IPR002396; -;
DR PRAM: PF00008; EGF_1.
DR PRAM: PF00059; lectin_c; 1.
DR PRAM: PF00084; sush1; 8.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS00186; EGF_2; 1.
DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE: PS00641; C-TYPE_LECTIN_2; 1.

KW Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sush1; Repeat; Lipoprotein; Palmitate.
FT SIGNAL 1 41
FT CHAIN 42 768
FT DOMAIN 42 709
FT TRANSMEM 710 733
FT DOMAIN 734 768
FT DOMAIN 58 158
FT DOMAIN 159 195
FT DOMAIN 199 700
FT REPEAT 199 258
FT REPEAT 261 320
FT REPEAT 323 382
FT REPEAT 385 444
FT REPEAT 447 506
FT REPEAT 509 568
FT REPEAT 579 638
FT REPEAT 641 700
FT DISULFID 60 158
FT DISULFID 131 150
FT DISULFID 163 174
FT DISULFID 168 183
FT DISULFID 185 194
FT DISULFID 200 244
FT DISULFID 230 257
FT DISULFID 262 306
FT DISULFID 292 319
FT DISULFID 324 368
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FT DISULFID 416 443
FT DISULFID 448 492
FT DISULFID 478 505
FT DISULFID 510 554
FT DISULFID 540 567
FT DISULFID 580 624
FT DISULFID 610 637
FT DISULFID 642 686
FT DISULFID 672 699
FT CARBOHYD 398 398
FT CARBOHYD 603 603
FT CARBOHYD 654 603
FT CARBOHYD 661 661
FT CARBOHYD 679 679
FT LIPID 745 745
FT SITE 756 759
FT CONFLICT 724 724
FT SEQUENCE 768 AA; 83098 MW; E5173074D2F66E68 CRC64;

Query Match 42.7%; Score 902.5; DB 1; Length 768;
Best Local Similarity 52.0%; Pred. No. 3.7e-64;
Matches 156; Conservative 40; Mismatches 103; Indels 1; Gaps 1;

OY 20 LMGWMLCCDCLAHNGVCTWYHYSEKPMNORAFCRDVTDLVATONKAETELYLKT 79
: : : : :
Db 24 IV-PSALISELYNOKEVAAWNTYINSTKAYSWNNSVFRFRIFTDLVATONKEIHLNDV 82
OY 80 LPEFSRYWIGIRKIGITWVGTKSLTEAEANGDEPNKKKEDCEVEITYKRKND 139
: : : : :
Db 83 IPEFSRYWIGIRKINNKWVGTKTLTEAEAMADNEPNKKKNOQCEVEITYKSNAP 142
OY 140 GKWMDACHKALCYTASQCPMSCHGECVELINNHGTCNDVGYGPOCQLYIOCEP 199
: : : : :
Db 143 GKWDEPCFKRRKALCYTASQCDMSCSNOGCEIETIGSYTCYGFYGPCEVYKECGK 202
OY 200 LEAPELGTMDCTHPGNGSFSQCAFSCSEGTNTLGIETTCGPFGNSSPEPTCOVYQC 259
: : : : :
Db 203 VNIRPOHVMNCSHPLGEFSFSQCTFCSCABEYELDGPPELOCLASGIWNTNPPCDAAQC 262
OY 260 EPLSAPDLGNCSPHLASFSFTSACTPFCSEGTETLGKRTTICSSGIMSNPSPICOKL 319
: : : : :
Db 263 QSLAPPHGTWACMHPILAAFAVDSCKRECPGYRANGSNTHGCGSGQWSEPLPTCAI 322

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RESULT 12
LEM3_BOVIN STANDARD; PRT; 646 AA.
ID LEM3_BOVIN
AC P42201;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
DE (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
GN SELP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eultheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CAPILLARY ENDOTHELIUM;
RX MEDLINE=93249394; PubMed=7683458;
RA Strubel N.A., Nguyen M., Kansas G.S., Tedder T.F., Bischoff J.;
RT "Isolation and characterization of a bovine cDNA encoding a
RL functional homolog of human P-selectin."
CC Biochem. Biophys. Res. Commun. 192:338-344(1993).
CC -1- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
CC TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
CC INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
CC LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS
CC AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
CC ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
CC THE CELL SURFACE.
CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMs.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS. BOVINE P-LECTIN LACKS
CC THE HUMAN SUSHI-3, -4 AND -7 EQUIVALENTS.
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CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L12041; AAA30743.1; -.
DR HSSP: P16109; IFSB.
DR INTERPRO: IPR000436; -.
DR INTERPRO: IPR000561; -.
DR INTERPRO: IPR001304; -.
DR INTERPRO: IPR002396; -.
DR PFAM: PF00008; EGF_1;
DR PFAM: PF00059; Lectin_C; 1.
DR PFAM: PF00084; SUSHI; 6.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE: PS00615; C-TYPE_LECTIN_2; 1.
DR Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; SUSHI; Repeat.
FT SIGNAL 1 41
FT CHAIN 42 646
FT DOMAIN 42 587
FT TRANSMEM 588 611
FT TRANSMEM 612 646
FT DOMAIN 58 158
FT DOMAIN 159 195
FT DOMAIN 199 258
FT REPEAT 199 258
FT REPEAT 261 320
SUSHI 1.
SUSHI 2.
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FT REPEAT 323 382
FT REPEAT 385 444
FT REPEAT 457 516
FT REPEAT 519 578
FT DISULFD 59 60
FT DISULFD 131 150
FT DISULFD 163 174
FT DISULFD 168 183
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FT DISULFD 416 443
FT DISULFD 458 502
FT DISULFD 488 515
FT DISULFD 520 564
FT DISULFD 550 577
FT CARBOHYD 48 48
FT CARBOHYD 54 54
FT CARBOHYD 80 80
FT CARBOHYD 180 180
FT CARBOHYD 212 212
FT CARBOHYD 219 219
FT CARBOHYD 336 336
FT CARBOHYD 481 481
FT CARBOHYD 532 532
FT CARBOHYD 539 539
FT CARBOHYD 557 557
FT SITE 634 637
SO SEQUENCE 646 AA; 71229 MW; 57391244627A6ACA CRC64;
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Query Match 42.3%; Score 894.5; DB 1; Length 646;
Best local Similarity 48.7%; Pred. No. 1,3e-63;
Matches 155; Conservative 51; Mismatches 109; Indels 3; Gaps 1;

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QY 2 IFPMKQOSTQORDIMNFKLMGWTMLCCDFLAHNGTYWTHYSEKPNMQRARRCRDNY 61
   8 IIMWR--PQRAVERIVOLLCSVLFEVINQKEVSAMTYHNSKTYSMNYSRAFCQKYY 64
DB TDVAIYNKNAEIEYEKTFPSRSTYWTGIRKIGIMWWTGINSUTREAEWDDGEPNN 121
62 TDVAIYNKNAEIEYEKTFPSRSTYWTGIRKIGIMWWTGINSUTREAEWDDGEPNN 121
   65 TDVAIYNKNAEIEYEKTFPSRSTYWTGIRKIGIMWWTGINSUTREAEWDDGEPNN 124
QY 122 KKKEDCVEIYIKRNKDKAMNDACHRLKAALCYTASCQPMSCSGHQECVEIINHTCN 181
   125 KRNQDCVEIYIKSLASRGKWNDEPCWKRKRALCYRASQPMSCSKQEGCIETIGNTCS 184
QY 182 CDVGYGPGQCOLVIOCEPLAEPLGELGTMDCTHPFGNFSFSSOCAPSGEGTNLTGIEETTC 241
   185 CYGFETGPECEYRECGFDLPQHYNMNCSDPLGNFSNSHSCSFHCAEGVALNPSFLFC 244
QY 242 GFGNWSPEPTQYIOCEPLASDPLGIMNCSHPLASFTSACTGTCSTGELIGKKT 301
   245 LASGIWTSPPQCAVAVQCPALKSPEQSGMSCVQSAEAFQHOSSCSFSCEGFALVGEVY 304
QY 302 ICESGINSNSPQCQKL 319
DB 305 HCTALGVMTAPYCKAL 322
```

```
RESULT 13
LEM3_RAT STANDARD; PRT; 768 AA.
ID LEM3_RAT
AC P96106;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
```


DE (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
GN SELP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=LUNG;
RC MEDLINE=9433817; PubMed=7520013;
RA Auchampach J.A., Oliver M.G., Anderson D.C., Manning A.M.;
RT "Cloning, sequence comparison and in vivo expression of the gene
encoding rat P-selectin."
RL Gene 145:251-255(1994).
CC -1- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
LEUKOCYTES. THE LIGAND RECOGNIZED IS STALTY-LEWIS X.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED: SPLEEN,
LUNG, BRAIN, LIVER, HEART, KIDNEY, THYMUS, SMALL INTESTINE.
CC -1- INDUCTION: ACUTE INFLAMMATION (PROBABLY).
CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMs.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS; RAT P-LECTIN LACKS THE
HUMAN SUSHI-2 EQUIVALENT.
CC -----
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entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L23088; AAA60325.1; -;
DR HSP; P16109; IFSB.
DR INTERPRO: IPR000436; -;
DR INTERPRO: IPR000561; -;
DR INTERPRO: IPR001304; -;
DR INTERPRO: IPR002396; -;
DR PFAM: PF00059; lectin_c; 1.
DR PFAM: PF00084; sush1; 8.
DR PRINTS: PRO0343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS0186; EGF_2; 1.
DR PROSITE: PS00615; C-TYPE_LLECTIN_1; 1.
DR PROSITE: PS50041; C-TYPE_LLECTIN_2; 1.
KM Cell adhesion: Transmembrane; Glycoprotein; EGF-like domain; Lectin;
FT Selectin; Signal; Sush1; Repeat; Lipoprotein; Palmitate.
FT SIGNAL 1 41
FT CHAIN 42 768
FT DOMAIN 42 709
FT TRANSMEM 710 733
FT DOMAIN 734 768
FT DOMAIN 58 158
FT DOMAIN 159 195
FT DOMAIN 199 258
FT REPEAT 199 258
FT REPEAT 261 320
FT REPEAT 323 382
FT REPEAT 385 444
FT REPEAT 447 506
FT REPEAT 509 568
FT REPEAT 579 638
FT REPEAT 641 700
FT DISULFID 60 158
FT DISULFID 131 150
FT DISULFID 168 183
FT DISULFID 185 194
FT DISULFID 200 244
FT DISULFID 230 257
FT DISULFID 262 306

FT DISULFID 292 319 BY SIMILARITY.
FT DISULFID 324 368 BY SIMILARITY.
FT DISULFID 354 381 BY SIMILARITY.
FT DISULFID 386 430 BY SIMILARITY.
FT DISULFID 416 442 BY SIMILARITY.
FT DISULFID 448 492 BY SIMILARITY.
FT DISULFID 478 505 BY SIMILARITY.
FT DISULFID 510 554 BY SIMILARITY.
FT DISULFID 540 567 BY SIMILARITY.
FT DISULFID 580 624 BY SIMILARITY.
FT DISULFID 610 637 BY SIMILARITY.
FT DISULFID 642 686 BY SIMILARITY.
FT DISULFID 672 699 BY SIMILARITY.
FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 107 107 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 456 456 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 603 603 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 654 654 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 661 661 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 679 679 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 745 745 PALMITATE (BY SIMILARITY).
FT SITE 756 759 ENDOTYROSIS SIGNAL (PROBABLE).
SQ SEQUENCE 768 AA; 83517 MW; 26FD78A5F3E1316 CRC64;

Query Match 41.8%; Score 885; DB 1; length 768;
Best Local Similarity 53.4%; Pred. No. 9e-63;
Matches 150; Conservative 42; Mismatches 89; Indels 0; Gaps 0;

QY 39 WYHNSKRRPMWQARRRCRRONTYDVALQKAELEYLEKTLPSRSYVWIGIRKIGIW 98
DB 42 WYVNSTKAYSMNNSRAKCRHFTDLVALQNKNEIHLNDYIPVANSYWIGIRINKW 101
QY 99 TWVGTKSLTEAEENWGDGEPNNKKNKEDVEIYIKRRKDGKWNDDCIHLKALCYTA 158
DB 102 TWVGTKNKTTLTAEEENWADNEPNKRNNDQVEIYIKSASAGKWNDECFKRRKALCYTA 161
QY 159 SCQWPCSGHGECVEIINNHTCNDVGYGPOCOLVIOCEPLEAPBELCTMDCTHPFGNFS 218
DB 162 SCQWPCSGHGECVEIINNHTCNDVGYGPOCOLVIOCEPLEAPBELCTMDCTHPFGNFS 221
QY 219 FSSQCAFSCSGTNTLTGIEFTTCGFGWSSPEPICOVIOCEPIASAPDLGTMNSHPLAS 278
DB 222 FSSQCFESCPGPGYDLNGPSEMOCLASGIVTNNPQCKAVOCOSLEAPLHGTMDCTHPLAA 281
QY 279 FSFISACFFICSEGTGLGKKKTKICSESGIWSNPSPICQKL 319
DB 282 FAYSSCKFECPGPRMRGSDILHCTDSGOWSEPLPTEAI 322

RESULT 14
ID LEM2_HUMAN STANDARD; PRT; 610 AA.
AC P16581; P16111;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-AUG-1990 (Rel. 15, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)
DE (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2)
DE (CD62E).
GN SELE OR ELAM1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90175359; PubMed=1689848;
RA Hession C., Osborn L., Goff D., Chi-Rosso G., Vassallo C.,
Pasek M., Plattack C., Tizard R., Goetz S., McCarthy K., Hopple S.,
Lobb R.;

FT	CARBOHYD	265	265	N-LINKED (GLCNAC. . .)	(POTENTIAL)					
FT	CARBOHYD	312	312	N-LINKED (GLCNAC. . .) <th>(POTENTIAL)</th>	(POTENTIAL)					
FT	CARBOHYD	332	332	N-LINKED (GLCNAC. . .) <th>(POTENTIAL)</th>	(POTENTIAL)					
FT	CARBOHYD	503	503	N-LINKED (GLCNAC. . .) <th>(POTENTIAL)</th>	(POTENTIAL)					
FT	CARBOHYD	527	527	N-LINKED (GLCNAC. . .) <th>(POTENTIAL)</th>	(POTENTIAL)					
FT	VARIANT	149	149	S -> R (ASSOCIATED WITH A RISK FACTOR FOR CAD) <td></td>						
FT				/FTID=VAR_004191.						
FT	CONFLICT	468	468	H -> Y (IN REF. 2).						
SO	SEQUENCE	610 AA;	66655 MW;	7D43E3C0D1229229 CRC64;						
Query Match										
Best Local Similarity		40.7%;	Score 862;	DB 1;	Length 610;					
Matches 145;		Conservative 41;	Mismatches 93;	Indels 0;	Gaps 0;					
Oy	WTYHSEKPMNOMRARRCRDNYDTGLVAINQNAELEYLEKTLPRFSRYWIGIRKIGIM 98									
Db	22 WSYNTSTEMNTYDEASVACQQRITLVAIQNKEELEYLSILSYSPSYIWIIRKYNW 81									
Oy	99 TWGYNKSLTEBAENMGDEEPNNKKNEKEDCELYIKRNKDAGKWNDDCKHLKALCYTA 158									
Db	82 VWVGQKPLTEBAKMMARAGEPRNNRQCKDKDCVEYTIKREDDGWNMDERCSKKKLACTA 141									
Oy	159 SCQPMSCSGHCECVETINNHTCNCDVGYGGPOCQLVIOCEPLEADELGTMDCTHPGNFS 218									
Db	142 ACTNNTSCSGHCECVETINNHTCKDCPCGFSGLKCEQIVACTALESPHSGSLVCSHPLGNS 201									
Oy	219 PSSOCAPFSCSEBTNLTGIEFTTCGPFQWMSSPREPCOYIOCEPLASAPDLGIMNCNHPLAS 278									
Db	202 YNNSOSISCDRDLPLDSMETMQMSSGGEASAIIPACNVEDCAVTNPANGVEYECFQNGS 261									
Oy	279 FSEFTACFFICSEGTGLGKKTKTIESSGIMSPAPICO 317									
Db	262 FPMNNTCFHDECEGFELMGAGOSLQCTSSGNDNENKPTCK 300									
RESULT 15										
LEM2_RABIT										
ID	LEM2_RABIT	STANDARD;		PRT;	551 AA.					
IC	P27113;									
DT	01-AUG-1992 (Rel. 23, Created)									
DT	01-AUG-1992 (Rel. 23, Last sequence update)									
DT	01-NOV-1997 (Rel. 35, Last annotation update)									
DE	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)									
DE	(ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2)									
DE	(CD62E).									
GN	SELE.									
OS	Oryctolagus cuniculus (Rabbit).									
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.									
RN	[1]									
RP	SEQUENCE FROM N.A.									
RC	TISSUE=HEART;									
RA	MEDLINE=92189729; PubMed=1372169;									
RA	Larigan J.D., Tsang T.C., Rumberger J.M., Burns D.K.;									
RT	"Characterization of cDNA and genomic sequences encoding rabbit									
RT	ELAM-1: conservation of structure and functional interactions with									
RT	Leukocytes.";									
RL	DNA Cell Biol. 11:149-162(1992).									
CC	-1 FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND									
CC	MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZED BY									
CC	ELAM-1 IS STALY-LWIS X (ALPHA1-3) PUCCOLATED DERIVATIVES OF									
CC	POLYACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF	GLYCOPOLIDS).								
CC	-1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.									
CC	-1 INDUCTION: BY CYTOKINES.									
CC	-1 SIMILARITY: TO OTHER SELECTINS/LECAMS.									
CC	-1 SIMILARITY: CONTAINS 1 C-TERM LECTIN FAMILY DOMAIN.									
CC	-1 SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.									
CC	-1 SIMILARITY: CONTAINS 5 SUSHI (SCR) REPEATS.									
CC	-----									
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration									

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CC	or send an email to license@sib-sib.ch)
DR	EMBL; M91004; AAA31243.1; -
DR	EMBL; M91005; AAA31244.1; -
DR	HSSP; P16581; IKJA.
DR	INTERPRO; IPR000436; -
DR	INTERPRO; IPR000561; -
DR	INTERPRO; IPR001304; -
DR	INTERPRO; IPR002396; -
DR	PFAM; PF00008; EGF_1.
DR	PFAM; PF00059; lectin_c.1.
DR	PFAM; PF00084; sushi_5.
DR	PRINTS; PR00343; SELECTIN.
DR	PROSITE; PS00022; EGF_1; 1.
DR	PROSITE; PS01186; EGF_2; 1.
DR	PROSITE; PS00615; C-TYPE LECTIN.1; 1.
DR	PROSITE; PS50041; C-TYPE LECTIN.2; 1.
KW	Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin; Selectin; Signal; Sushi; Repeat.
FT	SIGNAL 1 23
FT	CHAIN 24 551
FT	DOMAIN 24 495
FT	DOMAIN 496 517
FT	TRANSMEM 518 551
FT	DOMAIN 40 140
FT	DOMAIN 141 177
FT	DOMAIN 181 487
FT	REPEAT 181 240
FT	REPEAT 243 302
FT	REPEAT 305 365
FT	REPEAT 368 428
FT	REPEAT 431 487
FT	DISULFID 42 140
FT	DISULFID 113 132
FT	DISULFID 145 156
FT	DISULFID 150 165
FT	DISULFID 167 176
FT	DISULFID 182 226
FT	DISULFID 212 239
FT	DISULFID 244 288
FT	DISULFID 274 301
FT	DISULFID 306 351
FT	DISULFID 337 364
FT	DISULFID 369 414
FT	DISULFID 400 427
FT	DISULFID 432 473
FT	DISULFID 459 486
FT	CARBOHYD 32 32
FT	CARBOHYD 45 45
FT	CARBOHYD 162 162
FT	CARBOHYD 194 194
FT	CARBOHYD 201 201
FT	CARBOHYD 205 205
FT	CARBOHYD 267 267
FT	CARBOHYD 314 314
FT	CARBOHYD 321 321
FT	CARBOHYD 334 334
FT	CARBOHYD 442 442
FT	CARBOHYD 466 466
FT	CARBOHYD 308 308
FT	CONFLICT 328 328
FT	CONFLICT 491 491
SO	SEQUENCE 551 AA; 60346 MW; 23BC8A83B23240E CRC64;
Query Match	40.7%; Score 861; DB 1; length 551;
Best Local Similarity	51.8%; Pred. No. 5e-61;
Matches 146; Conservative 41; Mismatches 95; Indels 0; Gaps 0;	

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 13, 2001, 01:14:23 : Search time 77.13 seconds
(without alignments)
565.297 Million cell updates/sec

Title: US-09-119-209-2
Perfect score: 2116
Sequence: 1 MIFPMKOSTORDLWNIFKL.....MLARLKKGKSKSRMNDPY 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: SP.ROMUL_15:*
2: SP.ROMUL_15:*
3: SP.ROMUL_15:*
4: SP.ROMUL_15:*
5: SP.ROMUL_15:*
6: SP.ROMUL_15:*
7: SP.ROMUL_15:*
8: SP.ROMUL_15:*
9: SP.ROMUL_15:*
10: SP.ROMUL_15:*
11: SP.ROMUL_15:*
12: SP.ROMUL_15:*
13: SP.ROMUL_15:*
14: SP.ROMUL_15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2090	98.8	385	4 Q9UJ43	Q9UJ43 homo sapien
2	1796	84.9	376	6 Q28629	Q28629 oryctolagus
3	1667	78.8	372	11 Q63762	Q63762 ratulus norv
4	911	43.1	616	4 Q95509	Q95509 homo sapien
5	909	43.0	740	4 Q95507	Q95507 homo sapien
6	898	42.4	740	4 Q95508	Q95508 homo sapien
7	884	41.8	754	6 Q28290	Q28290 canis famli
8	876.5	41.4	646	6 Q29097	Q29097 sus scrofa
9	860.5	40.7	649	6 Q28657	Q28657 oryctolagus
10	815.5	38.5	482	6 Q28982	Q28982 sus scrofa
11	247.5	11.7	1124	5 Q9VXR4	Q9VXR4 drosophila
12	237.5	11.2	974	5 P91658	P91658 drosophila
13	236	11.2	868	5 Q18849	Q18849 caenorhabdi
14	216	10.2	1061	5 Q9VXX7	Q9VXX7 drosophila
15	199.5	9.4	449	4 Q14570	Q14570 homo sapien
16	199.5	9.4	449	4 Q9N086	Q9N086 homo sapien
17	199.5	9.4	1172	4 Q9N087	Q9N087 homo sapien
18	195	9.2	958	5 Q9V560	Q9V560 drosophila
19	189.5	9.0	1083	5 Q26423	Q26423 carcinoscor

20	183	8.6	328	4 Q9UJ71	Q9UJ71 homo sapien
21	176	8.3	378	6 Q62837	Q62837 saguinus oe
22	175.5	8.3	2014	6 Q29530	Q29530 pan troglod
23	174.5	8.2	1652	5 Q9VU9	Q9VU9 drosophila
24	172	8.1	2039	4 Q16745	Q16745 homo sapien
25	172	8.1	2489	4 Q16744	Q16744 homo sapien
26	171.5	8.1	395	12 Q9J2M6	Q9J2M6 macaca mula
27	171	8.1	354	5 Q9U611	Q9U611 drosophila
28	171	8.1	359	5 Q9V0X3	Q9V0X3 drosophila
29	170	8.0	314	6 Q62835	Q62835 saguinus oe
30	170	8.0	404	4 Q9NMX6	Q9NMX6 homo sapien
31	169.5	8.0	559	4 Q9UQV2	Q9UQV2 homo sapien
32	168	7.9	292	4 Q14538	Q14538 homo sapien
33	168	7.9	533	11 Q08569	Q08569 cavia porce
34	166	7.8	1911	6 Q29528	Q29528 papio hamad
35	165.5	7.8	560	5 Q22328	Q22328 caenorhabdi
36	165.5	7.8	1479	11 Q64449	Q64449 mus musculu
37	165	7.8	287	4 Q03969	Q03969 homo sapien
38	165	7.8	292	4 Q00448	Q00448 homo sapien
39	164.5	7.8	377	6 Q62838	Q62838 saguinus oe
40	164	7.8	214	11 Q9R008	Q9R008 mus musculu
41	164	7.8	339	11 P97261	P97261 cavia porce
42	164	7.8	661	6 Q29531	Q29531 pan troglod
43	163	7.7	269	5 Q24696	Q24696 dugesia tlig
44	163	7.7	669	6 Q28085	Q28085 bos taurus
45	162.5	7.7	379	11 P70105	P70105 cavia porce

ALIGNMENTS

RESULT 1	Q9UJ43	PRELIMINARY:	PRT: 385 AA.
ID	Q9UJ43		
AC	Q9UJ43		
DT	01-MAY-2000 (TRENBLREL. 13, Created)		
DT	01-MAY-2000 (TRENBLREL. 13, Last sequence update)		
DT	01-OCT-2000 (TRENBLREL. 15, Last annotation update)		
DE	L-SELECTIN PRECURSOR.		
GN	L-SELECTIN.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Gracilata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=HEMATOPOIETIC (B LYMPHOCYTE);		
RA	Fieger C.B.;		
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=HEMATOPOIETIC (B LYMPHOCYTE);		
RA	Fieger C.B.;		
RL	Thesis (1998), Freie Universitaet Berlin, Fachbereich Chemie.		
DR	EMBL: AJ246000; CAB55488.1; -		
DR	HSSP: P14151; IKB.		
DR	INTERPRO: IPR000436; -		
DR	INTERPRO: IPR000561; -		
DR	INTERPRO: IPR001304; -		
DR	INTERPRO: IPR002396; -		
DR	PFAM: PF00008; EGF_1.		
DR	PFAM: PF00059; Lectin_C_1.		
DR	PFAM: PF00084; sush1_2.		
DR	PRINTS: PR00343; SELECTIN.		
DR	PROSITE: PS00022; EGF_1; UNKNOWN_1.		
DR	PROSITE: PS00615; C-TYPE_LLECTIN_1; 1.		
DR	PROSITE: PS01186; EGF_2; 1.		
DR	PROSITE: PS50041; C-TYPE_LLECTIN_2; 1.		
KW	Signal; Lectin; Selectin.		
FT	SIGNAL		
FT	CHAIN		
SO	SEQUENCE		

Query Match	84.9%;	Score 1796;	DB 6;	Length 376;
Best Local Similarity	84.1%;	Pred. No. 5.1e-168;		

Query Match	78.8%;	Score 1667;	DB 11;	Length 372;
Best Local Similarity	77.2%;	Pred. No. 2.3e-155;		
Matches 287;	Conservative 35;	Mismatches 50;	Indels 0	

1 MIFPWKCOSTQRDLWNIFKLGWTMLCCDFLAHHGTYCWTYHYSSEKPMNWQRRARRECRDN 60

[illegible][illegible]

```

Db      191 GPECEYVRECEGELPLPOHVLNMCNCHPLGNFSFNOCSEFHCIDGYVNGSPKLECLASGIN 250
QY      248 SSPEPTCOVIOCEPLASPDGIMNCSHPLASFSTTSACTFTICSGTLLJCKKTKTCSSG 307
      251 TNKRPQCLAAOCPLKIPERGNMTCLHSAKAFQHSSCSFCEGFAVGVPEVVOCTASG 310
QY      308 IWSNPSPICOKL 319
      311 WTAAPAVCKAI 322

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```

RESULT 6
095508
ID      095508      PRELIMINARY;      PRT;      740 AA.
AC      095508;
DT      01-MAY-1999 (TREMBLrel. 10, Created)
DT      01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE      D1780M13.1.2 (SELECTIN P (GRANULE MEMBRANE PROTEIN 140 KDA, ANTIGEN
      CD62, GMP140)) (ISOFORM 2) (FRAGMENT).
GN      SELP.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Howden P.;
RL      Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AL022146; CAA18143.1; -.
DR      HSSP; P16109; 1KID.
DR      INTERPRO; IPR000436; -.
DR      INTERPRO; IPR000561; -.
DR      INTERPRO; IPR001304; -.
DR      INTERPRO; IPR002396; -.
DR      PFAM; PF00008; EGF_1.
DR      PFAM; PF00059; lectin.C; 1.
DR      PFAM; PF00084; sushi; 8.
DR      PRINTS; PR00343; SELECTIN.
DR      PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR      PROSITE; PS00615; C_Type_Lectin_1; 1.
DR      PROSITE; PS01186; EGF_2; 1.
DR      PROSITE; PS50041; C_Type_Lectin_2; 1.
FT      NON_TER
FT      CHAIN
FT      SIGNAL
SEQUENCE 740 AA; 81389 MW; 1D2E35EDD93745CE CRC64;

```

Query Match 42.4%; Score 898; DB 4; Length 740;
 Best Local Similarity 50.6%; Pred. No. 1.4e-79;
 Matches 158; Conservative 45; Mismatches 109; Indels 0; Gaps 0;

```

QY      8 OSQORDLMNIFKLMGWMMLCCDFLAHHGYCWTYHSEKPMNQARARFCRDNYTDLVAI 67
      11 ORFRVAVFGISQLCTFALISELTNOKEVAAMTYHSTKAYSWNISRKYCQNRHTDLVAI 70
Db      68 ONKAEIELEKTTLPFSRSYWGIRKIGITWYGNKSLTEAEAMNGOGEPPNNKKNKED 127
      71 ONKMEIDYLMKVLPEYSSYTWIGIRKNNKKTWVGTAKKALITAEAMWADENPNKKNKED 130
QY      128 CVELIYIRKNDAGKWDADACHKLKALCYTASQPMWCSGSGEGVEIINNHTCNCVGY 187
      131 CVELIYIKSPAPKWNDEHCLKKKHALCYTASQDMSCSKQGECLTIGNYTCSCIPGY 190
Db      191 GPCCOLATIOCEPLAPDLGTMDCTHPGNFSFSSQCAFSCECTNLGTIEFTTCGPFQNM 247
      191 GPCEYVRECEGELPLPOHVLNMCNCHPLGNFSFNOCSEFHCIDGYVNGSPKLECLASGIN 250
QY      248 SSPEPTCOVIOCEPLASPDGIMNCSHPLASFSTTSACTFTICSGTLLJCKKTKTCSSG 307
      251 TNKRPQCLAAOCPLKIPERGNMTCLHSAKAFQHSSCSFCEGFAVGVPEVVOCTASG 310
QY      308 IWSNPSPICOKL 319

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Db      311 HWSAPLPTCEAI 322

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RESULT 7
028290
ID      028290      PRELIMINARY;      PRT;      754 AA.
AC      028290;
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE      01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE      CELL ADHESION MOLECULE PRECURSOR (FRAGMENT).
GN      GMP140.
OS      Canis familiaris (Dog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX      NCBI_TaxID=9615;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Manning A.M., Sanders W.E. Jr., Kukielka G.L., Dore M.,
RA      Rosendloom C.L., Hawkins H.L., Michael L.H., Entman M.L., Smith C.W.,
RA      Beaudet A.L., Anderson D.C.;
RL      Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR      EMBL; M88170; AAA63789.1; -.
DR      HSSP; P16109; 1FSB.
DR      INTERPRO; IPR000436; -.
DR      INTERPRO; IPR000561; -.
DR      INTERPRO; IPR001304; -.
DR      INTERPRO; IPR002396; -.
DR      PFAM; PF00059; lectin.C; 1.
DR      PFAM; PF00084; sushi; 8.
DR      PRINTS; PR00343; SELECTIN.
DR      PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR      PROSITE; PS00615; C_Type_Lectin_1; 1.
DR      PROSITE; PS01186; EGF_2; 1.
DR      PROSITE; PS50041; C_Type_Lectin_2; 1.
KW      Signal; Cell adhesion; Glycoprotein.
FT      NON_TER
FT      SIGNAL
FT      CHAIN
FT      SIGNAL
SEQUENCE 754 AA; 82303 MW; F0438BEAA521E773 CRC64;

```

Query Match 41.8%; Score 884; DB 6; Length 754;
 Best Local Similarity 50.5%; Pred. No. 3.3e-78;
 Matches 151; Conservative 46; Mismatches 102; Indels 0; Gaps 0;

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QY      19 KLMGWMMLCCDFLAHHGYCWTYHSEKPMNQARARFCRDNYTDLVAIONKAEIELEK 78
      7 KLCFSVLIFELIKQKEVAGWYNNSTKAYSMNYSRIFCOKHYTDLVAIONKKEIATLND 66
QY      79 TLPSRSYWGIRKIGITWYGNKSLTEAEAMNGOGEPPNNKKNKEDCVELIYIRKND 138
      67 VLPYNSYTWIGIRKINDKRWVGTAKKALITAEAMWADENPNKKNKEDCVELIYIKSLA 126
QY      139 AGKWDADACHKLKALCYTASQPMWCSGSGEGVEIINNHTCNCVGYXPCQOLYIQCE 198
      127 PGKWNDEPCWKRRKRALCTYTASQDMSCSKQGECLTIGNYTCSCIPGYSECEYVRECEG 186
Db      199 PLEAELCTMDCTHPGNFSFSSQCAFSCECTNLGTIEFTTCGPFQNMSSPEPTCOVIO 258
      187 DFDLPLPOHVLNMCNCHPLGNFSFNOCSEFHCIDGYVNGSPKLECLASGTYWNNKPRCAV 246
QY      259 CEPISAPDLGIMNCSHPLASFSTTSACTFTICSGTLLJCKKTKTCSSGSIWNSPPIQ 317
      247 CPPLKTPQGSNCLHSAKAFQHSSCSFCEGFAVGVPEVVOCTASGIMWTAAPVCE 305
Db

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RESULT 8
029097
ID      029097      PRELIMINARY;      PRT;      646 AA.
AC      029097;

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DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE P-SELECTIN PRECURSOR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=AORTA.
RA Rollins S.A., Johnson K.K., Birks C.W., Matis L.A., Rother R.P.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=AORTA.
RA MEDLINE=20171534; PubMed=10706724;
RA Stocker C.J., Sugars K.L., Harari O.A., Landis R.C., Morley B.J.,
Haskard D.O.;
RT "TNF-alpha, IL-4, and IFN-gamma regulate differential expression of P-
and E-selectin expression by porcine aortic endothelial cells.";
RL J. Immunol. 164:3309-3315(2000).
DR EMBL: L39075; AAA79007.1; -.
DR EMBL: AF163766; AAF43272.1; -.
DR HSSP: P16109; IFSB.
DR INTERPRO: IPR000436; -.
DR INTERPRO: IPR000561; -.
DR INTERPRO: IPR001304; -.
DR INTERPRO: IPR002396; -.
DR PFAM: PF00008; EGF_1.
DR PFAM: PF00059; lectin_C_1.
DR PFAM: PF00084; sushi; 6.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
DR PROSITE: PS00615; C-TYPE_LECTIN_1; UNKNOWN_1.
DR PROSITE: PS50041; EGF_2; 1.
DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
DR SIGNAL: 1; 41 POTENTIAL.
KW Signal; lectin; Glycoprotein; Selectin.
FT CHAIN 1 41
FT SEQUENCE 42 646 P-SELECTIN.
SQ SEQUENCE 646 AA; 71127 MW; 3863f44afe09f0b6 CRC64;

Query Match 41.4%; Score 876.5; DB 6; Length 646;
Best Local Similarity 46.3%; Pred. No. 1,5e-77;
Matches 158; Conservative 48; Mismatches 124; Indels 11; Gaps 2;

DB 11 ORDLMNIFKLMGWTMLCCDPLAHNGHYCWTYHYSEKPMNQARARPCRDNYTDLVAIONK 70
14 QVSEFRVQLLEFVALISDLNOKGVAAMVYNTSAVSWNTSHVFCQRYPTDLVAIONK 73
QY 71 AEIYLEKTLDPFSRSYWGIRKGTGWTWGTNKSILTEAEENMGDEPNKKKKKDECEVE 130
DB 74 KEIAYLDVADIVYSSYWGIRKTKNNKTWGTGKTLTQENNAKKEPNESNNQDCEVE 133
QY 131 IYIKRNKADGKMDNACHIKLKAALCTYASCPMSGSGHGECEVEIINNHTCNCDVGYGPO 190
DB 134 MYIKSLAPKGMNDPEVCRRKRALCYTASCSSTCSKQGETETIGYTCYISGFFGPR 193
QY 191 QQLVIGCEPLAPBLGMDCTHPFGNFSFSSQCAFSCSEGTNLTCLETTTCGPGNMSSP 250
DB 194 CEYKKEGGEKRLPQYVLTNCSHPNGNSFNQCSFHCAEGVTLNGPSHLECLAGNWTMP 253
QY 251 EPTQGVIGCEPLASPDGIMNCSHPLASFSTSACTFTCSGTELLKKKIKICSSSGIMS 310
DB 254 PPOCVAAVQCPALSPKGNNAKCLHSEKAFQYQSSCNFSCEGVALVPEVVQACSGMWT 313
QY 311 NPSPICOKLKSFSMIKEGDYNPFLPIPAVAVTAF-SGLAF 350
DB 314 APYVCKAI-----ICEPLESPYRGSMDCFPSSRAF 344

RESULT 9

Q28657
ID Q28657 PRELIMINARY; PRT; 649 AA.
AC Q28657;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE P-SELECTIN.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Vora D.K., Fang Z., Liva S.M., Parham F., Watson A.D., Drake T.A.,
RA Territo M.C., Berliner J.A.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Marden C.H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U39446; AAA81385.1; -.
DR HSSP: P16109; IFSB.
DR INTERPRO: IPR000436; -.
DR INTERPRO: IPR000561; -.
DR INTERPRO: IPR001304; -.
DR INTERPRO: IPR002396; -.
DR PFAM: PF00008; EGF_1.
DR PFAM: PF00059; lectin_C_1.
DR PFAM: PF00084; sushi; 6.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; BGF_1; UNKNOWN_1.
DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE: PS50041; EGF_2; 1.
DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
KW Lectin; Glycoprotein.
SQ SEQUENCE 649 AA; 71755 MW; ECCD8C847B84BC31 CRC64;

Query Match 40.7%; Score 860.5; DB 6; Length 649;
Best Local Similarity 48.3%; Pred. No. 5.6e-76;
Matches 153; Conservative 53; Mismatches 104; Indels 9; Gaps 4;

QY 2 IFPKCOSTQORDLMNIFKLMGWTMLCCDPLAHNGHYCWTYHYSEKPMNQARARPCRDNY 61
DB 8 IWMNR---FQAVAVRTVQLLCEFSVLFEVINQKEVSMTYHSKTYSMNYSRAFCQKYY 64
QY 62 TDLVAIONKAEIYLEKTLDPFSRSYWGIRK---IGIWTWGTNKSILTEAEENMGDGE 118
DB 65 TDLVAIONKNEIDVLENTIPYNSYWGIRKDOQING--TWVG-NKMLTEAEENMADNE 121
QY 119 PNKKKNEDCEVEIYIKRKADGKNNDACHIKLKAALCTYASCPMSGSGHGECEVEIINN 178
DB 122 PNKKRNNDCEVEIYIKSLADGKNNDPEVCRRKRALCYTASCSQDMSCKQGETETIGNY 181
QY 179 TCNCDVGYGPOCQLVIGCEPLAPBLGMDCTHPFGNFSFSSQCAFSCSEGTNLTLGEE 238
DB 182 TCSQYRPGYGECEVEYRMAISLDRLQNHNMNSHPNGNSFNHSCSPICACGYALNGSE 241
QY 239 TTCGPFGNWSSPEPTCOYIGCEPLASPDGIMNCSHPLASFSTSACTFTCSGTELLGK 298
DB 242 LECIASGIMTSPQCVAAVQCPALSPKGNNAKCLHSEKAFQYQSSCNFSCEGFEIQLG 301
QY 299 KKTICESGIMSNPSICOKL 319
DB 302 EVVHCTALGVTAFTPVCKAL 322

RESULT 10
Q28982
ID Q28982 PRELIMINARY; PRT; 482 AA.
AC Q28982;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)

Query Match 38.5%; Score 815.5; DB 6; Length 482;
Best Local Similarity 36.1%; Pred. NO. 1e-71;
Matches 159; Conservative 56; Mismatches 109; Indels 117; Gaps 7;

RESULT	11	
Q9VYR4		
ID	Q9VYR4	PRELIMINARY;
AC	Q9VYR4;	PRT; 1124 AA
DT	01-MAY-2000	(TEMBLrel. 13, Created)

SEQUENCE FROM N.A
STRAIN=BERKELEY;
MEDLINE=20196006;
RX

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanosides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abil J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Betman B.P., Bhandari D., Bolstakov S.,
RA Borkova D., Bouchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burks J.C., Busam D.A., Butler H., Cadieu E., Cantor A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Pangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heilmann T.J., Hernandez J., Houck J.,
RA Hoston D., Houston K.A., Howland T.J., Mei M.-H., Idegyam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laspo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh C.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshiradi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Munz D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclik J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klimos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenhach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000)
DR EMBL: AE003487; AAF48125.1; -
DR HSSP: P02749; 10UB
DR FLYBASE: FBgn0001083; fw.
DR INTERPRO: IPR000436; -
DR INTERPRO: IPR001304; -
DR PfAM: PF00059; lectin_C; 1.
DR PFAM: PF00084; sushi; 11.
DR PROSITE: PS00615; C TYPE LECTIN_1; 1.
DR PROSITE: PSS0041; C TYPE LECTIN_2; 1.
SEQ 1124 AA; 123051 MW; COE0528A415F34A CRC64;

Query Match	11.7%;	Score 247.5;	DB 5;	Length 1124;
Best Local Similarity	25.5%;	Pred. No. 1.4e-15;		
Matches	86;	Conservative	40;	Mismatches 122.
				Indels 80.

QY 38 CWTYHSEKPMNMRARRFCNDNTYDVLAIQNKAEIYLEKTLPEFSR-----YYWGIR 92
 Db 231 CYDFHIT-KGEFFDAQAQICQGTGSDLVHDFRCATSSYLSELERKSKELPLQVLWIGAQ 269
 QY 93 KIGGI-----WTWVYGRKSLVEEAMNMDGEPNNKKKKECVETLYTKRKNDAK--WNDD 145

Db 230 KEPGITSFTKWKVNGD---VVQKPTWKGDPNNNGEONCVL-----DGGRNLMNDV 340
QY 146 ACHKLKALCYTASQCPWSCSGH-----GECVEIT-----NNHTC 180
Db 341 GCN--LDVLFHTICQHSPLSCGSPDAQONTYWGKKFTLGEKIQTICPFGHSLGTEREC 398
QY 181 NCDVGYVG--PQCOLVIOCEPLEAELGTMDCTHPFGNF-----SFSOCAFSCSECT 231
Db 399 RLDGTWSSSPTCKYV--DCGSL--PEL-----KFGSIHSEERTSFGVATYSCHENY 448
QY 232 NLTGIEFTTCPPFGWSSPEPTCOYIOC--EPLSAPLGLIMNCHPLASFSFT-----S 283
Db 449 TLIGENRTGCMADG--WSGKQPECLVDWCPDPPPIAGDV-----RFNDKRAGS 495
QY 284 ACTFICSECTELIGKKTKICSSGIMSNPSPICOKLD 320
Db 496 TATVCEGTYLVGHAITISCLGCGEMSSKTPSCRRVD 532

RESULT 12
P91658 PRELIMINARY; PRT; 974 AA.
AC P91658;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, last annotation update)
DE FURROWED.
CN FW.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN RN
RP SEQUENCE FROM N.A.
RA Leshko-Lindsay L., Corces V.G.;
RL Development 0:0-0(0).
DR EMBL: U70770; AAB36703.1; -;
DR HSSP: P02749; 10UB.
DR FLYBASE; FBgn0001083; fw.
DR INTERPRO: IPR000436; -;
DR INTERPRO: IPR001304; -;
DR PFAM: PF00059; lectin_c.1.
DR PFAM: PF00084; sushl; 10.
DR PROSITE: PS00615; C-type_lectin_1; UNKNOWN_1.
DR PROSITE: PS50041; C-type_lectin_2; 1.
SQ SEQUENCE 974 AA; 107537 MW; A406335FB6726757 CRC64;

Query Match 11.2%; Score 237.5; DB 5; Length 974;
Best Local Similarity 25.2%; Pred. No. 1,2e-14;
Matches 85; Conservative 39; Mismatches 124; Indels 89; Gaps 18;

QY 38 CWTYHYSEKPMNWDARRFCRDNTDLVAIONKAEIYELEKTLPEFSRS---YVWIGIR 92
Db 49 CYDFHIT-KGSEFQKQAIKQOTGHLVHDFRGATSSYILSELERRKSELKPQLWIIAQ 107
QY 93 KIGGI-----WTVVGTNKLTEAEENMGDEFPNNKKNKEDCEYIYIKRKKDAGK---WVND 145
Db 108 KEPGITSFTKWKVNGD---VVQKPTWKGDPNNNGEONCVL-----DGGRNLMNDV 158
QY 146 ACHKLKALCYTASQCPWSCSGH-----GECVEIT-----NNHTC 180
Db 159 GCN--LDVLFHTICQHSPLSCGSPDAQONTYWGKKFTLGEKIQTICPFGHSLGTEREC 216
QY 181 NCDVGYVG--PQCOLVIOCEPLEAELGTMDCTHPFGNF-----SFSOCAFSCSECT 231
Db 217 RLDGTWSSSPTCKYV--DCGSL--PEL-----KFGSIHSEERTSFGVATYSCHENY 266
QY 232 NLTGIEFTTCPPFGWSSPEPTCOYIOC--EPLSAPLGLIMNCHPLASFSFT-----S 283
Db 267 TLIGENRTGCMADG--WSGKQPECLVDWCPDPPPIAGDV-----RFNDKRAGS 313

QY 284 ACTFICSECTELIGKKTKICSSGIMSNPSPICOKLD 320
Db 314 TATVCEGTYLVGHAITISCLGCGEMSSKTPSCRRVD 350

RESULT 13
ID18849 PRELIMINARY; PRT; 868 AA.
AC Q18849;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, last annotation update)
DE C54G4.4 PROTEIN.
GN C54G4.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabdilitoidea;
OC Rhabdilitidae; Pelodierinae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN RN
RP SEQUENCE FROM N.A.
RA Wilkinson J.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN RN
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Lalster N., Latellie P.,
RA Lightling J., Lloyd C., Memurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkinson-Sprat J., Woldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
DR EMBL: Z75533; CA99822.1; -;
DR INTERPRO: IPR000436; -;
DR INTERPRO: IPR001304; -;
DR PFAM: PF00084; sushl; 4.
DR PROSITE: PS50041; C-type_lectin_2; 1.
SQ SEQUENCE 868 AA; 95322 MW; 5D57C332C70405CD CRC64;

Query Match 11.2%; Score 236; DB 5; Length 868;
Best Local Similarity 22.3%; Pred. No. 1,4e-14;
Matches 84; Conservative 48; Mismatches 128; Indels 116; Gaps 18;

QY 2 IFPMKQSTORDIANNIFPLMGWTLCDPLAHNGTCWTFYHSEKPMNWDARRFCRDNY 61
Db 339 VSPWQCAOSQMEVGVF-----GGMCTAASRDQ-TDWLQAQRKCLDRG 381
QY 62 TDVLAIONKAEIYELEKTLPEFS---RSYVWIGIRKIGIWTVGTNKLSTEEAENMGD-- 116
Db 382 STLPLRIDDSRRGLRSALSSASSAKAFYWGICASSMTEMWV-----DGEVYGSA 433
QY 117 ---GEPNNKKNKEDCEI-----YIKRNDAGKWDNDACHKLKALCYTASQCPWSCS 166
Db 434 DWPQSPSPVPSASEAVLLARLEWVKWVPASQTA--WNSFLQS-KPKRC-----TSP 482
QY 167 GHGECVEL-INNH-----C--NCDVY-----YGHQOLV 194
Db 483 GVGATYKVTFSHSAIGITLCIFYSDSGYDLHGIRQRCANGHWGTSIPNCRKSCAV 542
QY 195 IQCELEAELGTMDCTHPFGNF-----SFSOCAFSCSECTNLGIEFT----- 240
Db 543 RQWK-----FGRIKLNTTLTFESVEYTECGNWHLANSPPSYRSLRV 587
QY 241 CGPFGWSSPEPTCOYIOCEPLSAPLGLIMNCHPLASFSFTACTFICSECTELIGKK 300
Db 588 COSDGIWSSGSEPTCELVDG--GRPL-IANGRVDESSFTESANANTYCHQGFRIGPES 643

QY 301 TICSSGGLWNSPIC 316
 Db 644 LMGDRGEMOPATPFC 659

RESULT 14
 Q9VXX7
 ID Q9VXX7 PRELIMINARY; PRT; 1061 AA.
 AC Q9VXX7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE CG9095 PROTEIN.
 GN CG9095.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Phyllophaga; Drosophilidae; Drosophila.
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 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
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 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
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 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
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 RA Burris K.C., Busam D.A., Butler H., Cadenat E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kenton J.A., Ketchum K.A.,
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 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RL EMBL: AE003498; AAF48429.1; -;
 DR FLYBASE: FBgn0030617; CG9095.
 DR INTERPRO: IPR000436; -;
 DR INTERPRO: IPR001304; -;
 DR INTERPRO: IPR003006; -;
 DR PFAM: PF000059; lectin_c; 1.
 DR PFAM: PF000084; sushi; 3.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN.1.
 DR PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
 DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
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 QY 85 SYTWIGIRKIG---GIMTWV-GINKSLIEEENMGDGEPPNNKKKECCVEIYIKRNKDG 140
 Db 232 SQYMWGAVRQSDSSSMKWVNGDELIVSFWSHPGSD-----EDCARF-----DCS 276
 QY 141 K---WNDDACKRLAALCYTASQPSGSGHGE-----CVEIIN-----NH 178
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 QY 179 -----TNCNDVGYGC---PQCLVYQCEPLEAPELGTMDCIHP---FGNFS----- 218
 Db 333 LLVGPATRTTC-LETGFYNEPPVCKYI-----ECGLPASIAHGSYALLNNT 377
 QY 219 --FSSQAFSCSEGTNLTLGIEETCGPFGNWSPEPTCOVIOCEPLSAPDLG-IMNCSPH 275
 Db 378 VGYLSLVKYSCESEGYEMIGALLTCDPDERMNGPPPCCELVEDDTLPGNVSTIINA-P 435
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 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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 HE OR CFH.
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 RP SEQUENCE FROM N.A.
 RX MEDLINE=88134059; PubMed=2963625;
 RA Ripoché J., Day A.J., Harris T.J.R., Sim R.B.;
 RL "The complete amino acid sequence of human complement factor H.";
 RL Biochem. J. 249:593-602(1988).
 RN [2]
 RP SEQUENCE OF 226-449 FROM N.A.
 RX MEDLINE=86169701; PubMed=2937845;
 RA Kristensen T., Wetzel R.A., Jack B.F.;
 RL "Structural analysis of human complement protein H: homology with C4b binding protein, beta 2-glycoprotein I, and the Ba fragment of B2.";
 RL J. Immunol. 136:3407-3411(1986).
 RN [3]
 RP SEQUENCE OF 1-19 FROM N.A.
 RA Vik D.P., Williams S.A.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
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 RA Dominguez O.;
 RL Thesis (1993), Immunologia, Hospital Trias I Pujol, Spain.
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 DR EMBL: M12383; AAA52013.1; -;
 DR EMBL: U56979; AAB01987.1; -;
 DR HSSP: P10965; CA82763.1; -;
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 DR PFAM: PF000084; sushi; 7.
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 483)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TUMOR National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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www-bio.lhl.gov/bdrp/image/image.html
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T 3'); double-stranded cDNA was ligated to Eco RI
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the Not I and Eco RI sites of the modified p773 vector.
Library is normalized, and was constructed by Bento
Soares and M. Fatima Bonaldo."

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241 ysgLypProPheGlyAsnTrpSerSergProGluProThrCysGlnValIle 257
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381 GTGGACCATTTGGAAAGTGTATCTCCAGAACCACTGTACATGAT 332
258 .GlnCysGluProLeuSerAlaProAspleuGlyIleMetAsnCysSerH 274
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Baylor-HESC project=TCBA Homo sapiens cDNA clone TCBAPE1956, mRNA
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VERSION BE245855 GI:9097603
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 416)
AUTHORS Wei, Y., Tsang, Y.T.M., Wei, G., Ku, J.M., Ali-Osman Jr., F.R., Muzny, D.,
Bonck, J., Gibbs, R.A. and Margolin, J.F.
TITLE Pediatric Leukemia CDNA Sequencing Project

JOURNAL Unpublished (2000)
 COMMENT Contact: Dr. Judith F. Margolin
 Human Genome Sequencing Center at Baylor College of Medicine and
 Texas Children's Cancer Center
 One Baylor Plaza, Houston, TX 77030, USA
 Tel: 713 770 4536
 Fax: 713 770 4038
 Email: jmargin@tccc.org
 Seq primer: M13 primer.
 FEATURES Location/Qualifiers
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 3'; V-A,C,G; N-A,C,G,T] and then dg tailed. Second
 strand was primed with a BamHI-dc primer
 [5'AGAGCTCGATCGCGGCCGCAATATATATAT(C) 3'].
 Double-stranded cDNA was then digested with BamHI and
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 Yu"
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 164 CTTCAAGTTGGGGGTGGACAAATGCTGTGTGATTTCTGGGACATC 213
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 84 rGserTyTyTrpIleGlyIleArGlysIleGlyLylleTrpThrTrp 100
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 VERSION BE246681.1 GI:9098430
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 SOURCE human.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 421)
 AUTHORS Wei,Y., Tsang,Y.T.M., Mei,G., Xu,J.M., Ali-Osman Jr.,F.R., Muzny,D.,
 Bouck,J., Gibbs,R.A. and Margolin,J.F.
 TITLE Pediatric leukemia cDNA Sequencing Project
 JOURNAL Unpublished (2000)
 COMMENT Contact: Dr. Judith F. Margolin
 Human Genome Sequencing Center at Baylor College of Medicine and
 Texas Children's Cancer Center
 One Baylor Plaza, Houston, TX 77030, USA
 Tel: 713 770 4536
 Fax: 713 770 4038
 Email: jmargin@tccc.org
 Seq primer: M13 primer.
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 /lab_host="DH10B"
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 First strand cDNA was primed with an anchored
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 3'; V-A,C,G; N-A,C,G,T] and then dg tailed. Second
 strand was primed with a BamHI-dc primer
 [5'AGAGCTCGATCGCGGCCGCAATATATATAT(C) 3'].
 Double-stranded cDNA was then digested with BamHI and
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 Yu"
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 17 ePhelysLeuTrpGlyTrpThrMetLeuCyScAspPheLeuAlaIsh 34
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 164 CTTCAAGTTGGGGGTGGACAAATGCTGTGTGATTTCTGGGACATC 213


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314 ACAAAACAAAGCGCAATGTGATATCTGAGAGAACTCTCCCTTCAGTC 363
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KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 599)
Mambuit,R., Heubner,D., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Mambuit,et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Mambuit R

MIPI

Am KlopferSpitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
clone from S. Wiemann, Molecular Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by ACOMA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No s1 sequence available.

This clone (DKFZP586J1120) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

location/Qualifiers

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ACCESSION AA355761
VERSION AA355761.1 GI:2008079
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 293)

ADAMS M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wei,C., Clayton,R.A.,
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodok,A.,
Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,D.M.,
Kelley,J.C., Liu,L.-I., Marnaros,S.M., Merrick,J.M.,
Moreno-Palagunes,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Geol,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrite,A., Fischer,C., Hastings,G.A., He,W.W.,
Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L.,
Wel,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Pannon

```

145  |pAlaCysHlStLysLeuLysAlaAlaLeuCysTyrrThralaSerCysGlnp 162
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51  |GAGGTGCAGCAGAAAGACCTTGGCCCTATGCTACACAGCTCCTGTACCA 100
    |:::|  |||  |||  |||||||  |||||||  |||||||  |||
162  |roTrrSerCysSerGlyHlsglyGluCysValGluIleleAsnAsnHls 178
    ||||||  |||||||  |||||||  |||||||  |||||||  |||||||
101  |ATATACCTCGCGAGTGGCCAGCGTGATGTGTAGAGACCATTAAATTAATTC 150
    ||||||  |||||||  |||||||  |||||||  |||||||  |||||||
179  |ThrCysAsnCysAspValGlyTyrrTyrglyProGlnCysGlnLeuValI 195
    |:::|  |||  |||  |||  |||  |||  |||  |||  |||  |||
151  |ACTTCCAAAGTGTGACCCCTGCTCAGTGACTCAAGTGTGAGCAAAATTTGT 200
    |:::|  |||  |||  |||  |||  |||  |||  |||  |||  |||
195  |eGlnCysGluProLeuGluAlaProGluLeuGlyThrMetLaspCysThrH 212
    |:::|  |||  |||  |||  |||  |||  |||  |||  |||  |||
201  |GACGTGTACAGCCCTGGAATCCCTGAGCATGAGCAAGCCCTGTTGCGATC 250
    |:::|  |||  |||  |||  |||  |||  |||  |||  |||  |||
212  |sProPheGlyAsnPheSerPheSerSerGlnCysAlaPheSerCysSer 228
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251  |ACCCACTGGAACTTCAGTACAAATTTCTTCCTCATCAGCTGTGAT 300
    |:::|  |||  |||  |||  |||  |||  |||  |||  |||  |||
229  |GluGlyThrAsnLeuThrGlyIleGluGluThrThrCysGlyProPheG 245
    |:::|  |||  |||  |||  |||  |||  |||  |||  |||  |||
301  |AGGGTTACCTGCGCAAGCAGCATGAGACCATGACATGCTATGCTCTCTG 350
    |:::|  |||  |||  |||  |||  |||  |||  |||  |||  |||
245  |YAsnTrpSerSerProGluProThrCysGlnValIleGlnCysGluProL 262
    |:::|  |||  |||  |||  |||  |||  |||  |||  |||  |||
351  |AGATGTGAGTCTCTTATTCAGCTCTCAATGTGTGAGTGTGATCTGTCG 400
    |:::|  |||  |||  |||  |||  |||  |||  |||  |||  |||
262  |eUsrAlaProAspLeuGlyIleMetAsnCysSerHlsProLeuAlaSer 278
    |:::|  |||  |||  |||  |||  |||  |||  |||  |||  |||
401  |TGACAAATCCAGCCCAATGGGTGTGTGGAATTTCCAAACCTCGAAGC 450
    |:::|  |||  |||  |||  |||  |||  |||  |||  |||  |||
279  |PheSerPheThrSerAlaCysThrPheIleCysSerGluGlyThrGlu 295
    |:::|  |||  |||  |||  |||  |||  |||  |||  |||  |||
451  |TTCCATGAGAACACAACTGTGACATTTGACTGTGAAGAAGATTGAAC 500
    |:::|  |||  |||  |||  |||  |||  |||  |||  |||  |||
295  |uileGlyLysLysLysThrIleCysGluSerSerGlyIleTrpSerAsn 312
    |:::|  |||  |||  |||  |||  |||  |||  |||  |||  |||
501  |AATGGAGGCCAGCCAGCTTCAGTGTACCTCATCTGTGGAAATTGGAGAC 550
    |:::|  |||  |||  |||  |||  |||  |||  |||  |||  |||
312  |roSerProIleCysGln 317
    |:::|  |||  |||  |||  |||  |||  |||  |||  |||  |||
551  |NGAAGCCAAAGCTGTAA 567
    |:::|  |||  |||  |||  |||  |||  |||  |||  |||  |||

```

TITLE
JOURNAL
MEDLINE
COMMENT

.M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
96026280
Other_ESTs: TNC172390
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlavage@igf.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgl/hgl.html>)
Seq primer: M13 Reverse.
Location/Qualifiers
1. .293

FEATURES
source

/organism="Homo sapiens"
/db_xref="ATCC (lnhost):157887"
/db_xref="taxon:9606"
/clone_lib="Jurkat T-cells VI"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 70 a 71 c 75 g 74 t 3 others
ORIGIN

alignment_scores:
Quality: 547.00 Length: 97
Ratio: 5.758 Gaps: 0
Percent Similarity: 97.938 Percent Identity: 94.845

alignment_block:
US-09-119-209-2 x AA355761 ..

Align seg 1/1 to: AA355761 from: 1 to: 293

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160 CysGlnProTTPSerCysSerGlyHisGlyGlyCysValGluIleLeAs 176
|||||
3 TGCCAGCCCTGGTCATGCAGTGGCCATGNGAATGTGTAGANNATCAACAA 52
176 nasnhisthrcysasnrcysaspvalgltgtytrtyrclpProGlnCysGln 193
|||||
53 TAAATACACCTGCACCTGTGATGTGGGTACTATGGGCCCCACGTGTCACT 102
193 euvalilcGlnCysGlnProLeuGlnAlaProGlnLeuGlyThrMetAsp 209
|||||
103 TTGTGATTCAGGTGAGCGCTTTGGAGGCCCCAGAGCTGGGTACCTGAGNC 152
210 CysThrHisProPheGlyAsnProPheSerPheSerSerGlnCysAlaPheSe 226
|||||
153 TGTACTACACCCCTTTGGAAACTTCAGCTTCACAGTCACAGTGTGCTTCAG 202
226 rCysSerGlnGlyThrAsnLeuThrGlyTlGlnGlnLutThrCysGly 243
|||||
203 CTGCTCTGACAGCAACAACCTTAACCTGGATTGAGAAACACACCTCTTGAGC 252
243 rPheGlyAsnTrpSerSerProGlnProThrCysGlnVal 256
|||||
253 CATTTGGAAACTGCTCATCTCCAGAACCAACACCTGTCAAGTG 293

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seq_name: gb_est43:AW314314

seq_documentation_block:
LOCUS AW314314 382 bp mRNA EST 09-JUL-2000
DEFINITION 10316 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION AW314314
VERSION AW314314.1 GI:6743570
KEYWORDS EST.

SOURCE
ORGANISM
REFERENCE
AUTHORS

pig.
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
1 (bases 1 to 382)
Fahrenkrug,S.C., Fekling,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.M.
and Keeler,J.W.

TITLE
JOURNAL
COMMENT

Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 20
and -mismatch 12 options.

FEATURES
source

/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."

BASE COUNT 105 a 68 c 111 g 98 t

ORIGIN

alignment_scores:
Quality: 509.00 Length: 102
Ratio: 5.247 Gaps: 0
Percent Similarity: 95.098 Percent Identity: 81.373

alignment_block:
US-09-119-209-2 x AW314314 ..

Align seg 1/1 to: AW314314 from: 1 to: 382

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77 ATGATATTTCCATGGAATATGTCACAGTGTCTCAGAGGGCTTATGGAAATGT 126
17 ePheLysLeuTrpGlyTrpThrMetLeuCysCysAspPheLeuAlaHisN 34
|||||
127 CTTCAGAGTTGTGGGTCGTCGACATATGCTTTGTGTGATTTTGTTCATATC 176
34 lsgLThrTyrcysTrpThrTrpHisTyrSerGlnLysProMetAsnTrp 50
|||||
177 ATGGAACGTGATGCTGAGACTTACCACTATTCGAAACCCATGAACTCG 226
51 GlnArgAlaArgArgPheCysArgAspAsnTyrTrpAspLeuValAla11 67
|||||
227 ATGAGAGCTAGGAAGTTCTGTCAAGAAATTTACACAGATTTGTGCGCCT 276
67 eGlnAsnLysAlaGluIleGluTyrLeuGlnLutThrLeuProPheSerA 84
|||||
277 ACAAAACAAGGGGAGATTTGAATACCTGAAATTAAGACGCTTCCCTTCAGTC 326
84 rGSerTyrTyrTrpIleGlyIleArgLysIleGlyGlyTlLeTrpThrTrp 100
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327 GTAGTTACTACTGATAGGAATCCGGAAGGTGGAAGGGGTATGACATTGG 376

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101 ValGly 102
|||||
377 GTGGGA 382

seq_name: gb_est6:AA355250

seq_documentation_block:

LOCUS AA355250 297 bp mRNA EST 21-APR-1997
DEFINITION EST63788 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to
selectin L, mRNA sequence.

ACCESSION AA355250
VERSION AA355250.1 GI:2007715
KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 297)

Adams,M.D., Kerlavage,A.R., Fleschmann,R.D., Fuldner,R.A., Bult
,C.J., Lee,N.H., Kirkness,E.F., Weinstein,K.G., Gocayne,J.D., White
,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.,
Guelm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,
Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.,
Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L.,
Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon
,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
Venter,J.C.

TITLE

Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence

JOURNAL MEDLINE
96026280

COMMENT Other_ESTs: THC172390

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/db/hgl/hgl.html>)

Seq primer: M13 Reverse

Location/Qualifiers

Source

1..297

/organism="Homo sapiens"

/db_xref="ATCC (lnhost):157517"

/db_xref="taxon:9606"

/clone_lib="Jurkat T-cells VI"

/cell_type="T-lymphocyte"

/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:

XhoI"

BASE COUNT

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ORIGIN

alignment_scores:

Quality: 508.00 Length: 99

Ratio: 5.292 Gaps: 2

Percent Similarity: 96.970 Percent Identity: 93.939

alignment_block:

us-09-119-209-2 x AA355250 ..

align seg 1/1 to: AA355250 from: 1 to: 297

seq_name: gb_est6:AA361531

seq_documentation_block:

LOCUS AA361531 282 bp mRNA EST 21-APR-1997
DEFINITION EST70823 T-cell lymphoma Homo sapiens cDNA 5' end similar to
selectin L, mRNA sequence.

ACCESSION AA361531

VERSION AA361531.1 GI:2013852

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 282)

AUTHORS

Adams,M.D., Kerlavage,A.R., Fleschmann,R.D., Fuldner,R.A., Bult
,C.J., Lee,N.H., Kirkness,E.F., Weinstein,K.G., Gocayne,J.D., White
,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.,
Guelm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,
Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.,
Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L.,
Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon
,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
Venter,J.C.

TITLE

Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence

JOURNAL MEDLINE
96026280

COMMENT Other_ESTs: THC172390

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/db/hgl/hgl.html>)

Seq primer: M13 Reverse.

Location/Qualifiers'

FEATURES

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source
1. .282
/organism="Homo sapiens"
/db_xref="ATCC (inhost):165681"
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/clone_id="T-cell lymphoma"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

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ORIGIN

alignment_scores:
Quality: 501.00      Length: 92
Ratio: 5.505      Gaps: 0
Percent Similarity: 98.913      Percent Identity: 96.739

alignment_block:
US-09-119-209-2 x AA361531 ..

Align seg 1/1 to: AA361531 from: 1 to: 282

204 GUGUGGlyThrMetAspCysThrHisProphgIAsnPhseSerPhse 220
|||||
1 GAGCTGGGTAACCATGACTGACTCACCCTTGGGAACTTCACTGCGATTG 50
220 rSerGlnCysAlaPhseSerCysSerGlnGlyThrAsnLeuThrGlyIleG 237
|||||
51 CTCACAGTGTGCTTCAGTCTGCTGAGAGAACAACTTAACGGGATTG 100
237 luGluThrThrcysGlyProphgIAsnTrpSerSerProGluProThr 253
|||||
101 AAGAAACCAACCTGAGACCATTTGGAAACTGTCATCTCCAGAACCAAC 150
254 CysGlnValIleGlnCysGluProLeuSerAlaProAspLeuGlyIle 270
|||||
151 TGTCAGGATTCATCANTGTGACCTCTATCCAGCACAGATTGGGATCAT 200
270 tAsnGlySerHisProLeuAlaSerPhseSerPherThrSerAlaCysThr 287
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201 GAACGTGTACCATCCCTGCGCCAGCTTCACTTCACTTGCATGACT 250
287 heileCysSerGlnGlyThrGluLeu 295
|||||
251 TCATCTGCTCAGACAGAACTGAGGTT 276

seq_name: gb_est44:AM408490

seq_documentation_block:
LOCUS      AM408490      551 bp      mRNA      EST      16-FEB-2000
DEFINITION UT-HF-BKO-abm-g-01-0-UT.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3056832 5', mRNA sequence.
ACCESSION  AM408490
VERSION    AM408490.1 GI:6927547
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE     unpublished (1999)
JOURNAL   Contact: Robert Strausberg, Ph.D.
COMMENT   Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
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www.bio.lnlnl.gov/bdrrp/image/image.html
Seq primer: M13 Forward.
FEATURES
source
1. .551
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3056832"
/clone_id="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pTrf3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonafido, Ph.D., and M. Bento Soares, Ph.D."

BASE COUNT      162 a      124 c      106 g      159 t
ORIGIN

alignment_scores:
Quality: 496.00      Length: 94
Ratio: 5.277      Gaps: 0
Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-119-209-2 x AM408490 ..

Align seg 1/1 to: AM408490 from: 1 to: 551

279 PhseSerPheThrSerAlaCysThrPheileCysSerGlnGlyThrGlu 295
|||||
9 TTCAGCTTTTACCTCTGATGATGATCTTCACTGCTGCTGCAAGAACATGACGTT 58
295 uileGlyLysLysLysThrIleCysGlnSerSerGlyIleTrpSerAsp 312
|||||
59 AATTGGGAAGAAAGAAACCATTTGTCATCATCTGCAATCTGGTCAATTC 108
312 roSerProIleCysGlnLysLeuAspLysSerPhseSerMetIleLysGlu 328
|||||
109 CTAGTCCAAATATGTCCMAAATTTGACAAAGTTTTCATGATTAAGAG 158
329 GlyAspTrpAsnProLeuPheIleProValAlaValMetValThrAlaPh 345
|||||
159 GGTGATTAATACCCCTCTTCAATTCAGTGGCAGTCATGCTTACTGCAATT 208
345 eSerGlyLeuAlaPheIleIleTrpLeuAlaArgLeuLysGlyL 362
|||||
209 CTCTGGGTGGCATTTATCATTTGGGTGGCAGAGATTAAGGCA 258
362 yLysSerLysAspSerMetAsnAspProTyr 372
|||||
259 AGAAATCCCAAGAGAGATGATGATGATGATGATGATGATGATGATGAT 290

seq_name: gb_est39:AM075834

seq_documentation_block:
LOCUS      AM075834      632 bp      mRNA      EST      13-OCT-1999
DEFINITION x80C03.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2573092 3'
IMAGE:3056832 5', mRNA sequence.
ACCESSION  AM075834
VERSION    AM075834.1 GI:6030832
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE     Tumor Gene Index
```

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel.: (301) 496-1550
Email: Robert_C_Strausberg@nih.gov
Tissue Procurement: Elisabeth Paletta, Jonathan D. Licht, M.D.,
Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.linnl.gov/bbrp/lnage/lnage.html
Seq. primer: -400P from G13C0
High quality sequence stop: 147.

Location/Qualifiers
1. .632

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2573092"
/clone_id="NCI CGAP CML1"
/tissue_type="myeloid cells, 18 pooled CML cases, BCR/
rearrangement positive, includes both chronic phase and
myeloid blast crisis"
/lab_host="DH10B"
/notes="Organ: whole blood; Vector: pCMV-Sport6; Site_1:
SalI; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Library constructed by Life Technologies."
BASE COUNT
175 a 126 c 130 g 201 t

```

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alignment_scores:
  Quality: 452.00
  Ratio: 4.809
  Gaps: 0
Percent Similarity: 94.949
Percent Identity: 91.915
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alignment_block:

US-09-119-209-2 x AW075834/rev ..

Align seg 1/1 to reverse of: AM075834 from: 1 to: 632

271 AsncysSerHisProLeuAlaSerPheSerPheThrSerAlaCysThrPh 287
:::|||||
616 GACGTAGGCATCCCTGGCCAGCTCAGCTTACCTCGGAATTACTC 566
287 eIleCysSerGluGlyThrGlnLeuIleGlyLysLysLysThrIleCysG 304
567 .ATCTCTCAGAGGAACGATTAATTTGGAGAGAGAAACCATTTGTG 518
304 IuSerSerGlyLeuThrPheSerAsnProSerProIleCysGlnLysLeuAsp 320
517 AATCATCTCGAATCTGTCGTCGAATCTCATATGTCACAAATTTGCAC 468
321 LysSerPheSerMetIleLysGluGlyAspTyrAsnProLeuPheIlePr 337
467 AAAAGTTCTCATGATTAAAGGAGGGGTATTATTAACCCCTTCATTCC 418
337 oValAlaIaIaMetValThrAlaPheSerGlyLeuAlaPheIleIleTrpL 354
417 AGTGCGACGTCATGGTTACTGCATTCTCTGGGTTGGCATTTATCATTTGGC 368
354 euAlaIaArgLeuLysLysGlyLysLysSerLysArgSerMetAsn 369
367 TGCCAAAGGAGATTAAAAAAGCCAGGAAGATTCAGAGACAGATGAGAT 321

seq_name: gb_est6:AA355788

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seq_documentation_block:
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LOCUS	AA355788	346 bp	mrna	EST	21-APR-1997
DEFINITION	EST64242	Jurkat T-cells	VI Homo sapiens	CDNA 5' end	similar to
ACCESSION	U55570	selectin L,	mrna	sequence.	

VERSION : AA355788.1 GI:2008107

ORGANISM

Homo

Homo sapiens

AUTHORS

C.J., Lee, N.H., Kirkness, E.F., Weisskopf, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wei, C., Clayton, R.A., Lin, T.R., Cotton, M.D., Earle, Hughes, J., Fine, L.D., Fitzgarden, A., L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghegan, N.S., Glodok, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancques, R.F., McDonald, L.A., Nguyen, D.T., Pellagino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Sauder, D.M., Shirley, R., Small, R.V., Springs, T.A., Utterback, T.R., Weidman, J.F., Wiley, D., Bedark, D.P., Cao, L., Cepede, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferlie, A., Fischer, C., Haastings, G.A., He, M.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hunnig, J., Li, H., Melssner, P.S., Olsen, H., Raymond, L., Wel, Y.F., Wing, J., Xu, C., Yu, G., Ruben, S.M., Dillon, P.J., Pannoe, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

960268280

OTHER_ESTS: THCI172390

JOURNAL
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THE STATE OF
NEW YORK

JOURNAL
Nature 377 (6547 Suppl.), 3-174 (1995)
MEDLINE
96036280

Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlay@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/cdb/hgi.html>)
Seq primer: M13 Reverse.

Source

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/organism="Homo sapiens"
/db_xref="ATCC (inhost):157916"
/db_xref="taxon:9606"
/cloze_lib="jurkat T-cells VI"
/cell_type="T-lymphocyte"
/motif_vector:pbinscript SK-: Site_1: EcoRI, Site_2:
XhoI
BASE COUNT      102 a      75 c      86 g      80 t      3 others
ORIGIN

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alignment_scores

Quality:	437.00	Length:	8
Ratio:	5.675	Gaps:	1
Percent Similarity:	92.771	Percent Identity:	92.771

alignment_block:

Align seg 1/1 to: AA355788 from: 1 to: 346

1 Mel1aetheriotrprlyscysginserrthrlnaatgaspaleutrasu1 17
96 ATAAATTTTCCATGCAAAAGTCAGAGACACCAGAGAGCAATTATGAAACAT 14
17 ephelysleutprgltytrpthmelleaucsfysaphelenuh1ash 34
146 CTCGAGGTGTGGGGGTGGCAATGCTCTGTTGATATTTCTGGCACATC 19
34 isglythryrcysrprhrrhrrhstysrserglulyspfrometacsntrp 50
196 ATGAGAACCACTGCTGAGCACTTACCATTTTCTGAAAAAACCATATACCTGG 245

51 GlnARGLAlArGARpGhecysAcGAsPasrTYTThAspleuValalal 67
|||||
246 CAAAGGCTTGAAGATTTCTCCGAGACANTTTACACAGATTTTAACTTGCCAT 295
67 eglnAsnLysAlaGluIleGluTrIleu.GluLysThrIleuProPhe 82
|||||
296 ACANAAACANAGCGGAAATTTAGTATCTGGGAGANAGACTGCTCTTTT 342
seq_name: gb_est6:AA352567

seq_documentation_block:
LOCUS AA352567 459 bp mRNA EST 21-Apr-1997
DEFINITION AS160578 Activated T-cells XX Homo sapiens cDNA 5' end similar to
selectin L, mRNA sequence.
ACCESSION AA352567
VERSION AA352567.1 GI:2004887
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 459)
AUTHORS Adams,M.D., Kerlavage,A.R., Fletschmann,R.D., Fudner,R.A., Bull
C.J., Lee,N.H., Kikness,E.F., Weinstock,K.G., Gocayne,J.D., White
O., Sutton,G., Blake,J.A., Brandon,R.C., Man'wal,C., Clayton,R.A.,
Cline,T.R., Cotton,M.D., Parle-Hughes,J., Fine,L.D., Fitzgerald
L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodak,A.,
Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,
Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shibley,R.,
Smell,K.V., Spriggs,T.A., Uterback,T.R., Weldman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dirke,D., Feng,D.-F., Ferris,A., Fischer,C., Hastings,G.A., He,W.M.,
Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
Kunisch,C., HungJun,J., Li,H., Meltsner,P.S., Olsen,H., Raymond,L.,
Welch,F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon
M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547, Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT Other_ESTs: THC172390
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tcbl/ngi/ngi.html>)
Seq primer: M13 Reverse.
Location/Qualifiers
1..459
/organism="Homo sapiens"
/db_xref="ATCC (lnhost):152766"
/db_xref="taxon:9606"
/clone_id="Activated T-cells XX"
/cell_type="T-lymphocyte"
/dev_stage="adult"
/note="Vector: pBluescript SK-; site_1: EcoRI; site_2:
XhoI"

BASE COUNT 137 a 93 c 91 g 132 t 6 others
ORIGIN

alignment_scores:
Quality: 425.00 Length: 81
Ratio: 5.247 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-119-209-2 x AA352567 ..

Align seg 1/1 to: AA352567 from: 1 to: 459

292 G|YThGluLeu|leGlyLysLysLysThr|leGyGlnSerSerGly|I 308
|||||
3 GCAGCTGAGCTTAATTGGAAGAGAAACCAATTTGATCATCTCGAAT 52
308 e|rPSeAsnProSerPro|leGyGlnLysLysLeuA|pLysSerPheSer| 325
|||||
53 CTGGTCGAATCC|TACGCAATATGTC|AAAAATTGGACAA|AAAGTTTTC| 102
325 e|lleLysG|uG|Lys|Asp|Tyr|Asn|Pro|Leu|Phe|le|Pro|Val|Ala|Val|Met 341
|||||
103 TGATTAAGGAGGGGTGATTAATACCCCTCTCATTCACAGGACATG| 152
342 ValThAlaPheSerG|LysLeuAlaPhe|le|le|TrP|LeuAla|Arg|Arg| 358
|||||
153 GTTAC|TTCATCTCTG|GCGATTTATCATTTGCTG|CAAGAGAT| 202
358 u|LysLysG|LysLysSerLysArgSer|LeuAsn|Asp|Pro|Tyr 372
|||||
203 AAAAAGGCAAGCAATCC|AAGAAAGTATGATGAC|CATAT 245

seq_name: gb_est6:AA355982

seq_documentation_block:
LOCUS AA355982 279 bp mRNA EST 21-APR-1997
DEFINITION EST64486 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to
selectin L, mRNA sequence.
ACCESSION AA355982
VERSION AA355982.1 GI:2008322
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 279)
Adams,M.D., Kerlavange,A.R., Fleischmann,R.D., Fudner,R.A., Bult
,C.J., Lee,N.H., Klinkens,E.F., Weinstock,K.G., Gocayne,J.D., White
,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
,L.M., Fitzhugh,W.M., Fritchman,J.L., Georgagen,N.S., Glodok,A.,
Gnethu,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,
Kelley,J.C., Liu,L.-I., Marmaro,S.M., Merrick,J.M.,
Moreno-Palacios,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Uteback,T.R., Weidman,J.F., Li,Y.,
Behnark,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
DiMeo,D., Feng,D.-F., Ferlie,A., Fischer,C., Hastings,G.A., He,W.W.,
Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
Kunsch,C., Hungjun,J., Li,H., Melisner,P.S., Olsen,H., Raymond,L.,
Wel,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon
,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cdna sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT Other-ESTs: THC172390
Contact: Kerlavange, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3016699056
Fax: 3016699423
Email: arkerlavange@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

```

FEATURES                      Seq primer: M13 Reverse.
                               Location/Qualifiers
    source                      1..279
                                   /organism="Homo sapiens"
                                   /db_xref="taxon:9606"
                                   /db_xref="ATCC (inhost):158134"
                                   /clone_lib="Jurkat T-cells VI"
                                   /cell_type="T-lymphocyte"
                                   /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                   XhoI"
BASE COUNT      89 a      56 c      69 g      64 t      1 others
ORIGIN

alignment_scores:
    Quality: 423.00      Length: 73
    Ratio: 5.958      Gaps: 0
    Percent Similarity: 97.260      Percent Identity: 97.260

alignment_block:
US-09-119-209-2 x MA355982 ..

Align seg 1/1 to: AA355982 from: 1 to: 279

1 MettlepepPOTpLyScyGlnSerThrGlnArgAspLeuTPAsnI 17
|||||
52 ATGATATTTCATGGAATGTCAGACACCAGAGGAGCTTATGGAACAT 101
|||||
17 ephelystLeuTPpLyTPThrMetLeuCyScyAspPheLeuAlaHisH 34
|||||
102 CTTCAGATTGCGGGGTGGACATCTCTGTGTGATTTCCGCGACATC 151
|||||
34 isGlyThrTyrcySTpThrThyHisTySerGluLysProMetAsnTrp 50
|||||
152 ATGACACCGACTGCTGACTTACCATTTATCTGAAAAACCATGAACTGG 201
|||||
51 GlnArgAlaArgArgPheCySArgAspAsnTyTrhAspLeuValAlaI 67
|||||
202 CAAAGGGCTAGAAAGATTCTGCCGAGACATTAACAGATTAGTGCAT 251
|||||
67 eGlnAsnLysAlaGluIle 73
|||||
252 ACAAAACAAGCGCGAAATT 270

seq_name: gb_est68:BE241595

seq_documentation_block:
LOCUS      BE241595      365 bp      mRNA      EST      13-JUL-2000
DEFINITION TCAAP1E0689 Pediatric acute myelogenous leukemia cell (FAB M1)
            Baylor-HGSC project-TCAA Homo sapiens cDNA clone TCAAP0689, mRNA
            sequence.
ACCESSION  BE241595
VERSION    BE241595.1
KEYWORDS   GI:9093317
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 365)
            Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman Jr., F.R., Muzny, D.,
            Bouck, J., Gibbs, R.A. and Margolin, J.F.
            Pediatric Leukemia cDNA Sequencing Project
            Unpublished (2000)
            Contact: Dr. Judith F. Margolin
            Human Genome Sequencing Center at Baylor College of Medicine and
            Texas Children's Cancer Center
            One Baylor Plaza, Houston, TX 77030, USA
            Tel: 713 770 4536
            Fax: 713 770 4038
            Email: jmargin@bcm.tmc.org
            Seq primer: M13 primer.
FEATURES
    source                      Location/Qualifiers
    1..365

```

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TCAA0689"
/clone_lib="Pediatric acute myelogenous leukemia cell (FAB
M1) Baylor-HGSC project-TCAA"
/sex="male"
/tissue_type="Leukopheresis"
/cell_type="myeloid cell"
/dev_stage="pediatric 6 years"
/lab_host="DH10B"
/note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI;
First strand cDNA was primed with an anchored
XhoI-oligo(dT) primer (5'GACGACCTGACGCGCGCGGAGAGAG(T)VN
3'; V-A,C,G; N-A,C,G,T) and then dg tailed. Second
strand was primed with a BamHI-dC primer
(5'AGGAGCTCGATCCGCGCGCGCATATATATAT(C) 3').
Double-stranded cDNA was then digested with BamHI and XhoI
and directionally cloned into the BamHI and SalI sites of
lambda pSB vector. Library was constructed by Wei Yu"
normalization. Library was constructed by Wei Yu"
BASE COUNT      110 a      81 c      91 g      82 t      1 others
ORIGIN

alignment_scores:
    Quality: 416.00      Length: 71
    Ratio: 5.943      Gaps: 0
    Percent Similarity: 98.592      Percent Identity: 97.183

alignment_block:
US-09-119-209-2 x BE241595 ..

Align seg 1/1 to: BE241595 from: 1 to: 365

1 MettlepepPOTpLyScyGlnSerThrGlnArgAspLeuTPAsnI 17
|||||
152 ATGATATTTCATGGAATGTCAGACACCAGAGGAGCTTATGGAACAT 201
|||||
17 ephelystLeuTPpLyTPThrMetLeuCyScyAspPheLeuAlaHisH 34
|||||
202 CTTCAGATTGCGGGGTGGACATCTCTGTGTGATTTCCGCGACATC 251
|||||
34 isGlyThrTyrcySTpThrThyHisTySerGluLysProMetAsnTrp 50
|||||
252 ATGACACCGACTGCTGACTTACCATTTATCTGAAAAACCATGAACTGG 301
|||||
51 GlnArgAlaArgArgPheCySArgAspAsnTyTrhAspLeuValAlaI 67
|||||
302 CAAAGGGCTAGAAAGATTCTGCCGAGACATTAACAGATTAGTGCAT 351
|||||
67 eGlnAsnLysAla 71
|||||
352 ACAAAACAAGCGCG 364

```